GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 12, 2006, 16:10:19 ; Search time 71.5 Seconds
(without alignments)
30.726 Million cell updates/sec

Title: US-10-716-030-1
Perfect score: 24
Sequence: 1 LNRRA 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	100.0	7	8	ADI52979	Adi52979 Polysacch
2	24	100.0	11	5	ABG94362	Abg94362 Human tum
3	24	100.0	11	5	ABG80698	Abg80698 Human tum
4	24	100.0	11	8	ADI40738	Adi40738 Human TNF
5	24	100.0	14	6	ADA19860	Ada19860 TNFalpha
6	24	100.0	14	8	ADI40811	Adi40811 C-TNF-alp
7	24	100.0	16	6	ADA19837	Ada19837 TNFalpha
8	24	100.0	16	6	ADA19839	Ada19839 TNFalpha
9	24	100.0	16	6	ADA19856	Ada19856 TNFalpha
10	24	100.0	16	6	ADA19851	Ada19851 TNFalpha
11	24	100.0	16	6	ADA19833	Ada19833 TNFalpha
12	24	100.0	16	6	ADA19836	Ada19836 TNFalpha
13	24	100.0	17	6	ABR42094	Abr42094 Human tum
14	24	100.0	20	2	AAR05522	Aar05522 Tumour ne
15	24	100.0	21	2	AAR06807	Aar06807 Tumour ne
16	24	100.0	30	2	AAR05523	Aar05523 Tumour ne
17	24	100.0	30	2	AAR06804	Aar06804 Tumour ne
18	24	100.0	30	6	ADA19844	Ada19844 TNFalpha
19	24	100.0	30	6	ADA19845	Ada19845 TNFalpha
20	24	100.0	30	6	ADA19854	Ada19854 TNFalpha
21	24	100.0	30	6	ADA19847	Ada19847 TNFalpha
22	24	100.0	30	6	ADA19850	Ada19850 TNFalpha
23	24	100.0	30	6	ADA19858	Ada19858 TNFalpha
24	24	100.0	30	6	ADA19832	Ada19832 TNFalpha
25	24	100.0	30	6	ADA19827	Ada19827 TNFalpha
26	24	100.0	30	6	ADA19841	Ada19841 TNFalpha
27	24	100.0	30	7	ADK41113	Adk41113 Human tum
28	24	100.0	31	6	ADA19830	Ada19830 TNFalpha
29	24	100.0	31	6	ADA19849	Ada19849 TNFalpha
30	24	100.0	31	6	ADA19857	Ada19857 TNFalpha
31	24	100.0	31	6	ADA19838	Ada19838 TNFalpha
32	24	100.0	32	8	ABO58737	Abo58737 Human gen
33	24	100.0	35	7	ADK41079	Adk41079 Human tum
34	24	100.0	36	3	AAB38436	Aab38436 Fragment
35	24	100.0	51	4	AAE13097	Aae13097 Peptide #
36	24	100.0	51	5	AAG66035	Aag66035 Amino aci
37	24	100.0	51	8	ADL16846	Adl16846 BTL.010 p
38	24	100.0	51	8	ADU64356	Adu64356 Protein f
39	24	100.0	52	8	ADJ36285	Adj36285 Self-coal
40	24	100.0	69	3	AAG01730	Aag01730 Human sec
41	24	100.0	70	5	ABP34565	Abp34565 Human cyt
42	24	100.0	80	8	ADX72124	Adx72124 Plant ful
43	24	100.0	87	5	ABP34953	Abp34953 Human ORF
44	24	100.0	88	4	AAU52620	Aau52620 Propionib
45	24	100.0	88	6	ABM49139	Abm49139 Propionib

ALIGNMENTS

RESULT 1
ADI52979
ID ADI52979 standard; peptide; 7 AA.
XX
AC ADI52979;
XX
DT 06-MAY-2004 (first entry)
XX
DE Polysaccharide binding (PB) peptide #15.
XX
KW Drug delivery; polysaccharide binding; PB.
XX
OS Unidentified.
XX
PN US2003190364-A1.
XX
PD 09-OCT-2003.
XX
PF 01-APR-2003; 2003US-00405339.
XX
PR 01-APR-2002; 2002US-0369568P.
XX
PA (PANI/) PANITCH A.
PA (SEAL/) SEAL B.
XX
PI Panitch A, Seal B;
XX
DR WPI; 2004-069109/07.
XX
PT Composition useful for releasing therapeutic agent comprises a polymer
PT network, several polysaccharide binding polypeptides bound to the polymer
PT network and negatively charged polysaccharides bound to the polypeptides.
XX
PS Claim 9; SEQ ID NO 40; 33pp; English.
XX
CC The present invention provides compositions for drug delivery, comprising
CC a polymer network, several polysaccharide binding (PB) polypeptides and
CC negatively charged polysaccharides. The present sequence is
CC polysaccharide binding (PB) peptide.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 24; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5

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Db          1 LNRRA 5
```

RESULT 2
ABG94362
ID ABG94362 standard; peptide; 11 AA.
XX
AC ABG94362;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human tumour necrosis factor (TNF) epitope #2.
XX
KW Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
KW cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW vaccine; infectious disease.
XX
OS Homo sapiens.
XX
PN WO200256905-A2.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-IB000166.
XX
PR 19-JAN-2001; 2001US-0262379P.
PR 04-MAY-2001; 2001US-0288549P.
PR 05-OCT-2001; 2001US-0326998P.
PR 07-NOV-2001; 2001US-0331045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
PI Piossek C;
XX
DR WPI; 2002-627351/67.
XX
PT Molecular antigen array used in the production of vaccines for infectious
PT diseases.
XX
PS Disclosure; Page 82; 441pp; English.
XX
CC This invention relates to a novel ordered and repetitive antigen array
CC used in the production of vaccines for infectious diseases. The invention
CC also discloses a composition comprising a non-natural molecular scaffold
CC comprising a core particle selected from a core particle of a non-natural
CC origin and a core particle of natural origin and an organiser comprising
CC at least one first attachment site, where the organiser is connected to
CC the core particle by at least one covalent bond. Also disclosed is an
CC antigen or antigenic determinant with at least one second attachment
CC site, where the antigen or antigenic determinant is amyloid beta peptide
CC (Abeta1-42) or its fragment and where the second attachment site is
CC selected from an attachment site not naturally occurring with the antigen
CC or antigenic determinant and an attachment site naturally occurring with
CC the antigen or antigenic determinant, where the second attachment site is
CC capable of association through at least one non-peptide bond to the first
CC attachment site and where the antigen or antigenic determinant and the
CC scaffold interact through the association to form an ordered and
CC repetitive antigen array. The invention also comprises a coat protein
CC capable of forming a capsid which comprises mutant Qbeta coat proteins
CC having an amino acid sequence selected from five amino acid sequences
CC fully defined in the specification. The compounds of the invention may
CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC immunisation and as a vaccine. The present sequence represents a protein
CC sequence used to create the compositions of the invention
XX
SQ Sequence 11 AA;

```
  Query Match             100.0%;  Score 24;  DB 5;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db          5 LNRRA 9
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RESULT 3
ABG80698
ID ABG80698 standard; peptide; 11 AA.
XX
AC ABG80698;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human tumour necrosis factor 22-32 epitope.
XX
KW Molecular antigen array; vaccine; antigen; antimicrobial;
KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;
KW graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;
KW adult respiratory distress syndrome; ARDS; Crohn's disease;
KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
KW Grave's disease; systemic lupus erythematosus; osteoporosis;
KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
KW angioimmunoproliferative lymphadenopathy; immunoblastive lymphadenopathy;
KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
KW enterokinase; cysteine-containing linker.
XX
OS Homo sapiens.
XX
PN WO200256907-A2.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-IB000168.
XX
PR 19-JAN-2001; 2001US-0262379P.
PR 04-MAY-2001; 2001US-0288549P.
PR 05-OCT-2001; 2001US-0326998P.
PR 07-NOV-2001; 2001US-0331045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (NOVS) NOVARTIS PHARMA AG.
PA (MAUR/) MAURER P.
PA (LECH/) LECHNER F.
PA (ORTM/) ORTMANN R.
PA (LUEO/) LUEOEND R.
PA (STAU/) STAUFENBIEL M.
PA (FREY/) FREY P.
XX
PI Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
XX
DR WPI; 2002-636514/68.
XX
PT Molecular antigen array used in the production of vaccines for infectious
PT diseases.
XX
PS Disclosure; Page 82; 418pp; English.
XX
CC The invention relates to a composition comprising: (a) a non-natural
CC molecular scaffold comprising: (i) a core particle selected from: (1) a
CC core particle of a non-natural origin; and (2) a core particle of natural
CC origin; and (ii) an organiser comprising at least one first attachment
CC site, where the organiser is connected to the core particle by at least
CC one covalent bond; (b) an antigen or antigenic determinant with at least
CC one second attachment site, where the antigen or antigenic determinant is
CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
CC attachment site is selected from: (i) an attachment site not naturally
CC occurring with the antigen or antigenic determinant; and (ii) an
CC attachment site naturally occurring with the antigen or antigenic
CC determinant, where the second attachment site is capable of association
CC through at least one non-peptide bond to the first attachment site; and

CC where the antigen or antigenic determinant and the scaffold interact
CC through the association to form an ordered and repetitive antigen array.
CC Also included is a process for producing a non-naturally occurring
CC ordered and repetitive antigen array. The composition is used in
CC immunisation and as a vaccine for diseases such as influenza, graft
CC versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult
CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
CC gravis, immunoproliferative disease lymphadenopathy,
CC angioimmunoproliferative lymphadenopathy, immunoblastive lymphadenopathy,
CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
CC osteoporosis and infectious diseases. The present sequence is an antigen
CC for use in the array of the invention. The antigen is modified to posses
CC a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N-
CC or C-terminal linker peptide which serves as the attachment point to a
CC virus like particle or bacterial protein (the scaffold protein)
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 24; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 5 LNRRA 9

RESULT 4
ADI40738
ID ADI40738 standard; peptide; 11 AA.
XX
AC ADI40738;
XX
DT 22-APR-2004 (first entry)
XX
DE Human TNF-alpha peptide SEQ ID NO:29.
XX
KW virus-like particle; bacteriophage AP205; coat protein; cytostatic;
KW vaccine; gene therapy; cancer; allergy; asthma; TNF-alpha.
XX
OS Homo sapiens.
XX
PN WO2004007538-A2.
XX
PD 22-JAN-2004.
XX
PF 14-JUL-2003; 2003WO-EP007572.
XX
PR 17-JUL-2002; 2002US-0396126P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann MF, Tissot A, Pumpens P, Cielens I, Renhofa R;
XX
DR WPI; 2004-122882/12.
XX
PT New virus-like particle, useful for preparing a composition for treating
PT or preventing a disease e.g., cancer, allergy or asthma.
XX
PS Disclosure; SEQ ID NO 29; 170pp; English.
XX
CC The present invention describes a virus-like particle (I) which
CC comprises: (a) a protein having the 131-amino acid sequence of
CC bacteriophage AP205 coat protein or the mutant coat protein, see ADI40710
CC or ADI40712 respectively; or (b) a mutein of the protein of (a). Also
CC described: (1) a mutein of the recombinant protein having the 131-amino
CC acid sequence; (2) a vector for producing a AP205 virus like particle
CC comprising a nucleotide sequence being at least 80, 90, 95 or 99%
CC identical to that of the sequence comprising 3635 or 3613 bp or producing
CC a recombinant protein comprising a nucleotide sequence encoding a
CC polypeptide fused to a protein; (3) a pharmaceutical composition
CC comprising the composition and a carrier; (4) a process for producing a
CC non-naturally occurring, ordered and repetitive antigen array; (5) a
CC method of treating or preventing a disease, disorder or physiologic
CC conditions in an individual; (6) a nucleic acid molecule comprising 3635-
CC bp sequence; (7) a host cell containing a nucleic acid or a vector; and
CC (8) a method of producing the virus-like particle. (I) has cytostatic
CC activity, and can be used in vaccines, and in gene therapy. The virus-
CC like particle is useful for preparing a composition for treating or
CC preventing a disease e.g., cancer, allergy or asthma. The present
CC sequence represents a TNF-alpha peptide, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 24; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 5 LNRRA 9

RESULT 5
ADA19860
ID ADA19860 standard; peptide; 14 AA.
XX
AC ADA19860;
XX
DT 20-NOV-2003 (first entry)
XX
DE TNFalpha receptor binding peptide SEQ ID NO:34.
XX
KW molecular library; identification; detection; binding site;
KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;
KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;
KW TNFalpha receptor; tumour necrosis factor alpha receptor;
KW inflammatory disease; Crohn's disease; intestinal ulceration;
KW intestinal irritation.
XX
OS Synthetic.
XX
PN EP1279962-A1.
XX
PD 29-JAN-2003.
XX
PF 27-JUL-2001; 2001EP-00202879.
XX
PR 27-JUL-2001; 2001EP-00202879.
XX
PA (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI Slootstra JW, Puijk WC, Van Dijk E;
XX
DR WPI; 2003-259178/26.
XX
PT Producing molecular library for identifying binding site of tumor
PT necrosis factor-alpha, comprises providing the library with many
PT molecules produced by segmental linkage of nucleic acids or peptides.
XX
PS Disclosure; Page 22; 70pp; English.
XX
CC The present invention describes a method (M1) for producing a molecular
CC library for identifying or detecting a binding site of tumour necrosis
CC factor alpha (TNFalpha). (M1) comprises providing the library with
CC several molecules, and further generating at least one of the molecules
CC by linking a first segment to a second segment. Also described: (1) a
CC library (I) comprising several molecules comprising at least a first and
CC a second segment obtainable by (M1); (2) a solid support (II) comprising
CC (I); (3) a synthetic or binding molecule (III) comprising a binding site
CC identifiable or obtainable by using (I); and (4) determining (M2) a
CC minimally essential motif for a binding site, by generating a library of
CC test molecules, determining the binding activity of a binding molecule

CC with the test molecules, calculating the average binding activity of test
CC molecules present in the library comprising a certain motif, and
CC determining a motif with a high average binding activity of test
CC molecules comprising the motif. (M1) is useful for producing a molecular
CC library for identifying or detecting a binding site of TNFalpha. (I) is
CC useful for screening for a binding site of TNFalpha capable of
CC interacting with a binding molecule, by screening a library with at least
CC one potential binding molecule and detecting binding between a member of
CC the library and the potential binding molecule. The binding molecule
CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous
CC binding site. (I) and (II) are useful for identifying or obtaining a
CC synthetic molecule comprising a binding site of hTNFalpha, or a binding
CC molecule capable of binding to a binding site of hTNFalpha. (III) is
CC useful for interfering with or effecting binding to a binding molecule of
CC hTNFalpha. The molecular libraries produced by (M1) are useful for
CC detecting or screening for discontinuous binding sites, in particular in
CC relation to binding molecule-ligand interactions such as for e.g. protein
CC -protein, protein-nucleic acid and nucleic acid-nucleic acid
CC interactions. The identified peptide constructs are useful to develop new
CC ligands with agonistic or antagonistic activity for human TNFalpha
CC receptor action and are useful in control and prevention of an array of
CC diseases with (chronic) inflammatory components such as Crohn's disease
CC and other intestinal ulcerations or irritations. The present sequence
CC represents a TNFalpha receptor binding peptide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 24; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 7 LNRRA 11

RESULT 6
ADI40811
ID ADI40811 standard; peptide; 14 AA.
XX
AC ADI40811;
XX
DT 22-APR-2004 (first entry)
XX
DE C-TNF-alpha peptide mutant SEQ ID NO:102.
XX
KW virus-like particle; bacteriophage AP205; coat protein; cytostatic;
KW vaccine; gene therapy; cancer; allergy; asthma; TNF-alpha; mutant.
XX
OS Synthetic.
XX
PN WO2004007538-A2.
XX
PD 22-JAN-2004.
XX
PF 14-JUL-2003; 2003WO-EP007572.
XX
PR 17-JUL-2002; 2002US-0396126P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann MF, Tissot A, Pumpens P, Cielens I, Renhofa R;
XX
DR WPI; 2004-122882/12.
XX
PT New virus-like particle, useful for preparing a composition for treating
PT or preventing a disease e.g., cancer, allergy or asthma.
XX
PS Disclosure; SEQ ID NO 102; 170pp; English.
XX
CC The present invention describes a virus-like particle (I) which
CC comprises: (a) a protein having the 131-amino acid sequence of
CC bacteriophage AP205 coat protein or the mutant coat protein, see ADI40710
CC or ADI40712 respectively; or (b) a mutein of the protein of (a). Also
CC described: (1) a mutein of the recombinant protein having the 131-amino
CC acid sequence; (2) a vector for producing a AP205 virus like particle
CC comprising a nucleotide sequence being at least 80, 90, 95 or 99%
CC identical to that of the sequence comprising 3635 or 3613 bp or producing
CC a recombinant protein comprising a nucleotide sequence encoding a
CC polypeptide fused to a protein; (3) a pharmaceutical composition
CC comprising the composition and a carrier; (4) a process for producing a
CC non-naturally occurring, ordered and repetitive antigen array; (5) a
CC method of treating or preventing a disease, disorder or physiologic
CC conditions in an individual; (6) a nucleic acid molecule comprising 3635-
CC bp sequence; (7) a host cell containing a nucleic acid or a vector; and
CC (8) a method of producing the virus-like particle. (I) has cytostatic
CC activity, and can be used in vaccines, and in gene therapy. The virus-
CC like particle is useful for preparing a composition for treating or
CC preventing a disease e.g., cancer, allergy or asthma. The present
CC sequence represents a TNF-alpha mutant peptide, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 24; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 8 LNRRA 12

RESULT 7
ADA19837
ID ADA19837 standard; peptide; 16 AA.
XX
AC ADA19837;
XX
DT 20-NOV-2003 (first entry)
XX
DE TNFalpha receptor binding peptide SEQ ID NO:11.
XX
KW molecular library; identification; detection; binding site;
KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;
KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;
KW TNFalpha receptor; tumour necrosis factor alpha receptor;
KW inflammatory disease; Crohn's disease; intestinal ulceration;
KW intestinal irritation.
XX
OS Synthetic.
XX
PN EP1279962-A1.
XX
PD 29-JAN-2003.
XX
PF 27-JUL-2001; 2001EP-00202879.
XX
PR 27-JUL-2001; 2001EP-00202879.
XX
PA (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI Slootstra JW, Puijk WC, Van Dijk E;
XX
DR WPI; 2003-259178/26.
XX
PT Producing molecular library for identifying binding site of tumor
PT necrosis factor-alpha, comprises providing the library with many
PT molecules produced by segmental linkage of nucleic acids or peptides.
XX
PS Disclosure; Page 16; 70pp; English.
XX
CC The present invention describes a method (M1) for producing a molecular
CC library for identifying or detecting a binding site of tumour necrosis
CC factor alpha (TNFalpha). (M1) comprises providing the library with

CC several molecules, and further generating at least one of the molecules
CC by linking a first segment to a second segment. Also described: (1) a
CC library (I) comprising several molecules comprising at least a first and
CC a second segment obtainable by (M1); (2) a solid support (II) comprising
CC (I); (3) a synthetic or binding molecule (III) comprising a binding site
CC identifiable or obtainable by using (I); and (4) determining (M2) a
CC minimally essential motif for a binding site, by generating a library of
CC test molecules, determining the binding activity of a binding molecule
CC with the test molecules, calculating the average binding activity of test
CC molecules present in the library comprising a certain motif, and
CC determining a motif with a high average binding activity of test
CC molecules comprising the motif. (M1) is useful for producing a molecular
CC library for identifying or detecting a binding site of TNFalpha. (I) is
CC useful for screening for a binding site of TNFalpha capable of
CC interacting with a binding molecule, by screening a library with at least
CC one potential binding molecule and detecting binding between a member of
CC the library and the potential binding molecule. The binding molecule
CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous
CC binding site. (I) and (II) are useful for identifying or obtaining a
CC synthetic molecule comprising a binding site of hTNFalpha, or a binding
CC molecule capable of binding to a binding site of hTNFalpha. (III) is
CC useful for interfering with or effecting binding to a binding molecule of
CC hTNFalpha. The molecular libraries produced by (M1) are useful for
CC detecting or screening for discontinuous binding sites, in particular in
CC relation to binding molecule-ligand interactions such as for e.g. protein
CC -protein, protein-nucleic acid and nucleic acid-nucleic acid
CC interactions. The identified peptide constructs are useful to develop new
CC ligands with agonistic or antagonistic activity for human TNFalpha
CC receptor action and are useful in control and prevention of an array of
CC diseases with (chronic) inflammatory components such as Crohn's disease
CC and other intestinal ulcerations or irritations. The present sequence
CC represents a TNFalpha receptor binding peptide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 24; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 9 LNRRA 13

RESULT 8
ADA19839
ID ADA19839 standard; peptide; 16 AA.
XX
AC ADA19839;
XX
DT 20-NOV-2003 (first entry)
XX
DE TNFalpha receptor binding peptide SEQ ID NO:13.
XX
KW molecular library; identification; detection; binding site;
KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;
KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;
KW TNFalpha receptor; tumour necrosis factor alpha receptor;
KW inflammatory disease; Crohn's disease; intestinal ulceration;
KW intestinal irritation.
XX
OS Synthetic.
XX
PN EP1279962-A1.
XX
PD 29-JAN-2003.
XX
PF 27-JUL-2001; 2001EP-00202879.
XX
PR 27-JUL-2001; 2001EP-00202879.
XX
PA (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI Slootstra JW, Puijk WC, Van Dijk E;
XX
DR WPI; 2003-259178/26.
XX
PT Producing molecular library for identifying binding site of tumor
PT necrosis factor-alpha, comprises providing the library with many
PT molecules produced by segmental linkage of nucleic acids or peptides.
XX
PS Disclosure; Page 17; 70pp; English.
XX
CC The present invention describes a method (M1) for producing a molecular
CC library for identifying or detecting a binding site of tumour necrosis
CC factor alpha (TNFalpha). (M1) comprises providing the library with
CC several molecules, and further generating at least one of the molecules
CC by linking a first segment to a second segment. Also described: (1) a
CC library (I) comprising several molecules comprising at least a first and
CC a second segment obtainable by (M1); (2) a solid support (II) comprising
CC (I); (3) a synthetic or binding molecule (III) comprising a binding site
CC identifiable or obtainable by using (I); and (4) determining (M2) a
CC minimally essential motif for a binding site, by generating a library of
CC test molecules, determining the binding activity of a binding molecule
CC with the test molecules, calculating the average binding activity of test
CC molecules present in the library comprising a certain motif, and
CC determining a motif with a high average binding activity of test
CC molecules comprising the motif. (M1) is useful for producing a molecular
CC library for identifying or detecting a binding site of TNFalpha. (I) is
CC useful for screening for a binding site of TNFalpha capable of
CC interacting with a binding molecule, by screening a library with at least
CC one potential binding molecule and detecting binding between a member of
CC the library and the potential binding molecule. The binding molecule
CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous
CC binding site. (I) and (II) are useful for identifying or obtaining a
CC synthetic molecule comprising a binding site of hTNFalpha, or a binding
CC molecule capable of binding to a binding site of hTNFalpha. (III) is
CC useful for interfering with or effecting binding to a binding molecule of
CC hTNFalpha. The molecular libraries produced by (M1) are useful for
CC detecting or screening for discontinuous binding sites, in particular in
CC relation to binding molecule-ligand interactions such as for e.g. protein
CC -protein, protein-nucleic acid and nucleic acid-nucleic acid
CC interactions. The identified peptide constructs are useful to develop new
CC ligands with agonistic or antagonistic activity for human TNFalpha
CC receptor action and are useful in control and prevention of an array of
CC diseases with (chronic) inflammatory components such as Crohn's disease
CC and other intestinal ulcerations or irritations. The present sequence
CC represents a TNFalpha receptor binding peptide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 24; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 4 LNRRA 8

RESULT 9
ADA19856
ID ADA19856 standard; peptide; 16 AA.
XX
AC ADA19856;
XX
DT 20-NOV-2003 (first entry)
XX
DE TNFalpha receptor binding peptide SEQ ID NO:30.
XX
KW molecular library; identification; detection; binding site;
KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;
KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;
KW TNFalpha receptor; tumour necrosis factor alpha receptor;

KW inflammatory disease; Crohn's disease; intestinal ulceration;
KW intestinal irritation.
XX
OS Synthetic.
XX
PN EP1279962-A1.
XX
PD 29-JAN-2003.
XX
PF 27-JUL-2001; 2001EP-00202879.
XX
PR 27-JUL-2001; 2001EP-00202879.
XX
PA (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI Slootstra JW, Puijk WC, Van Dijk E;
XX
DR WPI; 2003-259178/26.
XX
PT Producing molecular library for identifying binding site of tumor
PT necrosis factor-alpha, comprises providing the library with many
PT molecules produced by segmental linkage of nucleic acids or peptides.
XX
PS Disclosure; Page 21; 70pp; English.
XX
CC The present invention describes a method (M1) for producing a molecular
CC library for identifying or detecting a binding site of tumour necrosis
CC factor alpha (TNFalpha). (M1) comprises providing the library with
CC several molecules, and further generating at least one of the molecules
CC by linking a first segment to a second segment. Also described: (1) a
CC library (I) comprising several molecules comprising at least a first and
CC a second segment obtainable by (M1); (2) a solid support (II) comprising
CC (I); (3) a synthetic or binding molecule (III) comprising a binding site
CC identifiable or obtainable by using (I); and (4) determining (M2) a
CC minimally essential motif for a binding site, by generating a library of
CC test molecules, determining the binding activity of a binding molecule
CC with the test molecules, calculating the average binding activity of test
CC molecules present in the library comprising a certain motif, and
CC determining a motif with a high average binding activity of test
CC molecules comprising the motif. (M1) is useful for producing a molecular
CC library for identifying or detecting a binding site of TNFalpha. (I) is
CC useful for screening for a binding site of TNFalpha capable of
CC interacting with a binding molecule, by screening a library with at least
CC one potential binding molecule and detecting binding between a member of
CC the library and the potential binding molecule. The binding molecule
CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous
CC binding site. (I) and (II) are useful for identifying or obtaining a
CC synthetic molecule comprising a binding site of hTNFalpha, or a binding
CC molecule capable of binding to a binding site of hTNFalpha. (III) is
CC useful for interfering with or effecting binding to a binding molecule of
CC hTNFalpha. The molecular libraries produced by (M1) are useful for
CC detecting or screening for discontinuous binding sites, in particular in
CC relation to binding molecule-ligand interactions such as for e.g. protein
CC -protein, protein-nucleic acid and nucleic acid-nucleic acid
CC interactions. The identified peptide constructs are useful to develop new
CC ligands with agonistic or antagonistic activity for human TNFalpha
CC receptor action and are useful in control and prevention of an array of
CC diseases with (chronic) inflammatory components such as Crohn's disease
CC and other intestinal ulcerations or irritations. The present sequence
CC represents a TNFalpha receptor binding peptide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 24; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 8 LNRRA 12

RESULT 10
ADA19851
ID ADA19851 standard; peptide; 16 AA.
XX
AC ADA19851;
XX
DT 20-NOV-2003 (first entry)
XX
DE TNFalpha receptor binding peptide SEQ ID NO:25.
XX
KW molecular library; identification; detection; binding site;
KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;
KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;
KW TNFalpha receptor; tumour necrosis factor alpha receptor;
KW inflammatory disease; Crohn's disease; intestinal ulceration;
KW intestinal irritation.
XX
OS Synthetic.
XX
PN EP1279962-A1.
XX
PD 29-JAN-2003.
XX
PF 27-JUL-2001; 2001EP-00202879.
XX
PR 27-JUL-2001; 2001EP-00202879.
XX
PA (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI Slootstra JW, Puijk WC, Van Dijk E;
XX
DR WPI; 2003-259178/26.
XX
PT Producing molecular library for identifying binding site of tumor
PT necrosis factor-alpha, comprises providing the library with many
PT molecules produced by segmental linkage of nucleic acids or peptides.
XX
PS Disclosure; Page 20; 70pp; English.
XX
CC The present invention describes a method (M1) for producing a molecular
CC library for identifying or detecting a binding site of tumour necrosis
CC factor alpha (TNFalpha). (M1) comprises providing the library with
CC several molecules, and further generating at least one of the molecules
CC by linking a first segment to a second segment. Also described: (1) a
CC library (I) comprising several molecules comprising at least a first and
CC a second segment obtainable by (M1); (2) a solid support (II) comprising
CC (I); (3) a synthetic or binding molecule (III) comprising a binding site
CC identifiable or obtainable by using (I); and (4) determining (M2) a
CC minimally essential motif for a binding site, by generating a library of
CC test molecules, determining the binding activity of a binding molecule
CC with the test molecules, calculating the average binding activity of test
CC molecules present in the library comprising a certain motif, and
CC determining a motif with a high average binding activity of test
CC molecules comprising the motif. (M1) is useful for producing a molecular
CC library for identifying or detecting a binding site of TNFalpha. (I) is
CC useful for screening for a binding site of TNFalpha capable of
CC interacting with a binding molecule, by screening a library with at least
CC one potential binding molecule and detecting binding between a member of
CC the library and the potential binding molecule. The binding molecule
CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous
CC binding site. (I) and (II) are useful for identifying or obtaining a
CC synthetic molecule comprising a binding site of hTNFalpha, or a binding
CC molecule capable of binding to a binding site of hTNFalpha. (III) is
CC useful for interfering with or effecting binding to a binding molecule of
CC hTNFalpha. The molecular libraries produced by (M1) are useful for
CC detecting or screening for discontinuous binding sites, in particular in
CC relation to binding molecule-ligand interactions such as for e.g. protein
CC -protein, protein-nucleic acid and nucleic acid-nucleic acid
CC interactions. The identified peptide constructs are useful to develop new
CC ligands with agonistic or antagonistic activity for human TNFalpha
CC receptor action and are useful in control and prevention of an array of
CC diseases with (chronic) inflammatory components such as Crohn's disease
CC and other intestinal ulcerations or irritations. The present sequence

CC represents a TNFalpha receptor binding peptide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 24; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 2 LNRRA 6

RESULT 11
ADA19833
ID ADA19833 standard; peptide; 16 AA.
XX
AC ADA19833;
XX
DT 20-NOV-2003 (first entry)
XX
DE TNFalpha receptor binding peptide SEQ ID NO:7.
XX
KW molecular library; identification; detection; binding site;
KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;
KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;
KW TNFalpha receptor; tumour necrosis factor alpha receptor;
KW inflammatory disease; Crohn's disease; intestinal ulceration;
KW intestinal irritation.
XX
OS Synthetic.
XX
PN EP1279962-A1.
XX
PD 29-JAN-2003.
XX
PF 27-JUL-2001; 2001EP-00202879.
XX
PR 27-JUL-2001; 2001EP-00202879.
XX
PA (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI Slootstra JW, Puijk WC, Van Dijk E;
XX
DR WPI; 2003-259178/26.
XX
PT Producing molecular library for identifying binding site of tumor
PT necrosis factor-alpha, comprises providing the library with many
PT molecules produced by segmental linkage of nucleic acids or peptides.
XX
PS Disclosure; Page 15; 70pp; English.
XX
CC The present invention describes a method (M1) for producing a molecular
CC library for identifying or detecting a binding site of tumour necrosis
CC factor alpha (TNFalpha). (M1) comprises providing the library with
CC several molecules, and further generating at least one of the molecules
CC by linking a first segment to a second segment. Also described: (1) a
CC library (I) comprising several molecules comprising at least a first and
CC a second segment obtainable by (M1); (2) a solid support (II) comprising
CC (I); (3) a synthetic or binding molecule (III) comprising a binding site
CC identifiable or obtainable by using (I); and (4) determining (M2) a
CC minimally essential motif for a binding site, by generating a library of
CC test molecules, determining the binding activity of a binding molecule
CC with the test molecules, calculating the average binding activity of test
CC molecules present in the library comprising a certain motif, and
CC determining a motif with a high average binding activity of test
CC molecules comprising the motif. (M1) is useful for producing a molecular
CC library for identifying or detecting a binding site of TNFalpha. (I) is
CC useful for screening for a binding site of TNFalpha capable of
CC interacting with a binding molecule, by screening a library with at least
CC one potential binding molecule and detecting binding between a member of
CC the library and the potential binding molecule. The binding molecule
CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous
CC binding site. (I) and (II) are useful for identifying or obtaining a
CC synthetic molecule comprising a binding site of hTNFalpha, or a binding
CC molecule capable of binding to a binding site of hTNFalpha. (III) is
CC useful for interfering with or effecting binding to a binding molecule of
CC hTNFalpha. The molecular libraries produced by (M1) are useful for
CC detecting or screening for discontinuous binding sites, in particular in
CC relation to binding molecule-ligand interactions such as for e.g. protein
CC -protein, protein-nucleic acid and nucleic acid-nucleic acid
CC interactions. The identified peptide constructs are useful to develop new
CC ligands with agonistic or antagonistic activity for human TNFalpha
CC receptor action and are useful in control and prevention of an array of
CC diseases with (chronic) inflammatory components such as Crohn's disease
CC and other intestinal ulcerations or irritations. The present sequence
CC represents a TNFalpha receptor binding peptide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 24; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 1 LNRRA 5

RESULT 12
ADA19836
ID ADA19836 standard; peptide; 16 AA.
XX
AC ADA19836;
XX
DT 20-NOV-2003 (first entry)
XX
DE TNFalpha receptor binding peptide SEQ ID NO:10.
XX
KW molecular library; identification; detection; binding site;
KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;
KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;
KW TNFalpha receptor; tumour necrosis factor alpha receptor;
KW inflammatory disease; Crohn's disease; intestinal ulceration;
KW intestinal irritation.
XX
OS Synthetic.
XX
PN EP1279962-A1.
XX
PD 29-JAN-2003.
XX
PF 27-JUL-2001; 2001EP-00202879.
XX
PR 27-JUL-2001; 2001EP-00202879.
XX
PA (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI Slootstra JW, Puijk WC, Van Dijk E;
XX
DR WPI; 2003-259178/26.
XX
PT Producing molecular library for identifying binding site of tumor
PT necrosis factor-alpha, comprises providing the library with many
PT molecules produced by segmental linkage of nucleic acids or peptides.
XX
PS Disclosure; Page 16; 70pp; English.
XX
CC The present invention describes a method (M1) for producing a molecular
CC library for identifying or detecting a binding site of tumour necrosis
CC factor alpha (TNFalpha). (M1) comprises providing the library with
CC several molecules, and further generating at least one of the molecules
CC by linking a first segment to a second segment. Also described: (1) a
CC library (I) comprising several molecules comprising at least a first and

CC a second segment obtainable by (M1); (2) a solid support (II) comprising
CC (I); (3) a synthetic or binding molecule (III) comprising a binding site
CC identifiable or obtainable by using (I); and (4) determining (M2) a
CC minimally essential motif for a binding site, by generating a library of
CC test molecules, determining the binding activity of a binding molecule
CC with the test molecules, calculating the average binding activity of test
CC molecules present in the library comprising a certain motif, and
CC determining a motif with a high average binding activity of test
CC molecules comprising the motif. (M1) is useful for producing a molecular
CC library for identifying or detecting a binding site of TNFalpha. (I) is
CC useful for screening for a binding site of TNFalpha capable of
CC interacting with a binding molecule, by screening a library with at least
CC one potential binding molecule and detecting binding between a member of
CC the library and the potential binding molecule. The binding molecule
CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous
CC binding site. (I) and (II) are useful for identifying or obtaining a
CC synthetic molecule comprising a binding site of hTNFalpha, or a binding
CC molecule capable of binding to a binding site of hTNFalpha. (III) is
CC useful for interfering with or effecting binding to a binding molecule of
CC hTNFalpha. The molecular libraries produced by (M1) are useful for
CC detecting or screening for discontinuous binding sites, in particular in
CC relation to binding molecule-ligand interactions such as for e.g. protein
CC -protein, protein-nucleic acid and nucleic acid-nucleic acid
CC interactions. The identified peptide constructs are useful to develop new
CC ligands with agonistic or antagonistic activity for human TNFalpha
CC receptor action and are useful in control and prevention of an array of
CC diseases with (chronic) inflammatory components such as Crohn's disease
CC and other intestinal ulcerations or irritations. The present sequence
CC represents a TNFalpha receptor binding peptide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 24; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 1 LNRRA 5

RESULT 13
ABR42094
ID ABR42094 standard; peptide; 17 AA.
XX
AC ABR42094;
XX
DT 28-JUL-2003 (first entry)
XX
DE Human tumour necrosis factor-alpha external surface loop AA.
XX
KW Human; tumour necrosis factor-alpha; RANKL; osteopathic; bone.
XX
OS Homo sapiens.
XX
PN WO2003033663-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US033022.
XX
PR 15-OCT-2001; 2001US-0329393P.
XX
PA (BARN-) BARNES-JEWISH HOSPITAL.
XX
PI Lam J, Ross PF, Teitelbaum SL;
XX
DR WPI; 2003-430346/40.
XX
PT New RANKL mimic comprising a core, and at least one external loop, useful
PT for enhancing processes of bone formation or inhibiting bone resorption,
PT thus providing treatments for disease or condition characterized by loss
PT of bone mass.
XX
PS Disclosure; Page 15; 78pp; English.
XX
CC The present sequence is that of the AA" external surface loop of human
CC tumour necrosis factor (TNF)-alpha. The invention provides non-naturally-
CC occurring proteins that contain one or more of the external surface loops
CC of RANKL in combination with a heterologous protein core obtained from a
CC non-RANKL member of the TNF superfamily. Thus, the present external loop
CC sequence is replaceable by a RANKL external loop sequence. Such proteins
CC bind to RANK, acting as mimics of RANKL, and can be used to enhance bone
CC formation by either inhibiting bone resorption or inducing osteogenesis,
CC thus providing treatments for diseases or conditions characterised by
CC loss of bone mass
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 24; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 11 LNRRA 15

RESULT 14
AAR05522
ID AAR05522 standard; protein; 20 AA.
XX
AC AAR05522;
XX
DT 25-MAR-2003 (revised)
DT 24-OCT-1990 (first entry)
XX
DE Tumour necrosis factor derived peptide.
XX
KW Tumour necrosis factor; TNF; neoplastic disease; autoimmune disease;
KW infection; inflammation; transplant rejection.
XX
OS Synthetic.
XX
PN DE3841767-A.
XX
PD 13-JUN-1990.
XX
PF 12-DEC-1988; 88DE-03841767.
XX
PR 12-DEC-1988; 88DE-03841767.
XX
PA (BADI) BASF AG.
PA (BOEH/) BOEHM H J.
XX
PI Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;
XX
DR WPI; 1990-186583/25.
XX
PT Peptide tumour necrosis factor analogues - used in treatment of tumours
PT and auto:immune diseases.
XX
PS Example 16; Page 8; 16pp; German.
XX
CC To residue V1 is attached AcH and to residue A20 NH2. This peptide is an
CC example of a highly generic sequence of the formula X-A-B-E-Leu-Y A= Glu,
CC Pro or Gln; B= Gly, Glu, Asn or Asp; E= Gln or Ser; X= G-NH-CHM-CO, G-NH-
CC CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W; Y= Z, NH-CHQ-COZ, V-NH-CHQ-
CC COZ, NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z; G= H or a protecting group; Z= OH,
CC NH2 or carboxy protecting group; or G and Z together are a covalent bond
CC or the gp. CO(CH2)aNH; a=1-12; R and U= peptide chains of 1-5 naturally
CC occuring alpha aminoacids; W= one of the following dodecapeptide chains:
CC kpvahvvanpqa, kpvahvvadins, kplahvvanpqv, kpvahvvanhqv, kpaahligdpsk,
CC kpaahlvgdpst, kpaahlvgypsk. or a partial sequence of 5-11 amino acids
CC from one of the chains, or a peptide chain of 1-4 naturally occurring

```
CC   alpha amino acids; V= one of the following dodecapeptide chains:
CC   qwlnrranalla, rwwdsyanalma, qwlsqranalla, ewlsqranalla, lwrantdraflq,
CC   rwrantdraflr, lwrastdraflr. or a partial sequence of 5-11 amino acids
CC   from one of the chains, or a peptide chain of 1-4 natural alpha amino
CC   acids; M and Q= H, isopropyl, sec-butyl, phenyl, 1-hydroxyethyl, 3-
CC   indolyl, 4-imidazoly-methyl or (CH2)bT; b=1-6; T= OH, MeO, MeS,
CC   isopropyl, phenyl (opt. 4-OH, substd), mercapto, amino, carboxy,
CC   carbamoyl or quanidino; or M ans Q together are (CH2)c-S-S-(CH2)d,
CC   (CH2)eCO NH-(CH2)f or (CH)2eNH CO(CH2)gNH CO(CH2) f; c and d=1-4; e and
CC   f=1-6; g=1-12. The peptide is a low mol. wt. deriv. of TNF. See also
CC   DE3841753-55, DE3841759, DE3841761-64, DE3841767-68. (Updated on 25-MAR-
CC   2003 to correct PA field.)
XX
SQ   Sequence 20 AA;

  Query Match             100.0%;  Score 24;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         14 LNRRA 18


RESULT 15
AAR06807
ID   AAR06807 standard; protein; 21 AA.
XX
AC   AAR06807;
XX
DT   25-MAR-2003  (revised)
DT   24-OCT-1990  (first entry)
XX
DE   Tumour necrosis factor derived peptide.
XX
KW   Tumour necrosis factor; TNF; neoplastic disease; autoimmune disease;
KW   infection; inflammation; transplant rejection; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 21. .21
FT                   /label= OTHER
FT                   /note= "Ahx"
XX
PN   DE3841767-A.
XX
PD   13-JUN-1990.
XX
PF   12-DEC-1988;   88DE-03841767.
XX
PR   12-DEC-1988;   88DE-03841767.
XX
PA   (BADI ) BASF AG.
PA   (BOEH/) BOEHM H J.
XX
PI   Bohm HJ,  Daum L,  Haupt A,  Schmied B,  Walker N,  Zechel JC;
XX
DR   WPI; 1990-186583/25.
XX
PT   Peptide tumour necrosis factor analogues - used in treatment of tumours
PT   and auto:immune diseases.
XX
PS   Example 59; Page 13; 16pp; German.
XX
CC   This peptide is an example of a highly generic sequence of the formula X-
CC   A-B-E-Leu-Y A= Glu, Pro or Gln; B= Gly, Glu, Asn or Asp; E= Gln or Ser;
CC   X= G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W; Y= Z, NH
CC   -CHQ-COZ, V-NH-CHQ-COZ, NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z; G= H or a
CC   protecting group; Z= OH, NH2 or carboxy protecting group; or G and Z
CC   together are a covalent bond or the gp. CO(CH2)aNH; a=1-12; R and U=
CC   peptide chains of 1-5 naturally occuring alpha aminoacids; W= one of the
CC   following dodecapeptide chains: kpvahvvanpqa, kpvahvvadins, kplahvvanpqv,
CC   kpvahvvanhqv, kpaahligdpsk, kpaahlvgdpst, kpaahlvgypsk. or a partial
CC   sequence of 5-11 amino acids from one of the chains, or a peptide chain
CC   of 1-4 naturally occurring alpha amino acids; V= one of the following
CC   dodecapeptide chains: qwlnrranalla, rwwdsyanalma, qwlsqranalla,
CC   ewlsqranalla, lwrantdraflq, rwrantdraflr, lwrastdraflr. or a partial
CC   sequence of 5-11 amino acids from one of the chains, or a peptide chain
CC   of 1-4 natural alpha amino acids; M and Q= H, isopropyl, sec-butyl,
CC   phenyl, 1-hydroxyethyl, 3-indolyl 4-imidazoly-methyl or (CH2)bT; b=1-6;
CC   T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd), mercapto, amino,
CC   carboxy, carbamoyl or quanidino; or M ans Q together are (CH2)c-S-S-
CC   (CH2)d, (CH2)eCO NH-(CH2)f or (CH)2eNH CO(CH2)gNH CO(CH2) f; c and d=1-4;
CC   e and f=1-6; g=1-12. The peptide is a low mol. wt. deriv. of TNF. See
CC   also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68. (Updated on 25-
CC   MAR-2003 to correct PA field.)
XX
SQ   Sequence 21 AA;

  Query Match             100.0%;  Score 24;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         14 LNRRA 18


Search completed: January 12, 2006, 16:16:22
Job time : 72.5 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 12, 2006, 16:12:40 ; Search time 19 Seconds
(without alignments)
21.757 Million cell updates/sec

Title: US-10-716-030-1
Perfect score: 24
Sequence: 1 LNRRA 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	100.0	19	1	US-08-107-235-9	Sequence 9, Appli
2	24	100.0	19	1	US-08-178-268-43	Sequence 43, Appl
3	24	100.0	19	2	US-08-714-960B-9	Sequence 9, Appli
4	24	100.0	19	2	US-09-598-784-9	Sequence 9, Appli
5	24	100.0	51	2	US-09-369-494-16	Sequence 16, Appl
6	24	100.0	51	2	US-09-358-569D-14	Sequence 14, Appl
7	24	100.0	51	2	US-09-569-670-16	Sequence 16, Appl
8	24	100.0	69	2	US-09-513-999C-5811	Sequence 5811, Ap
9	24	100.0	71	2	US-09-632-287A-20	Sequence 20, Appl
10	24	100.0	71	2	US-10-286-696-20	Sequence 20, Appl
11	24	100.0	99	2	US-09-314-268-133	Sequence 133, App
12	24	100.0	104	2	US-09-911-777-5	Sequence 5, Appli
13	24	100.0	139	1	US-07-994-469A-10	Sequence 10, Appl
14	24	100.0	145	1	US-07-994-469A-9	Sequence 9, Appli
15	24	100.0	147	1	US-07-668-517-1	Sequence 1, Appli
16	24	100.0	147	2	US-09-105-343A-9	Sequence 9, Appli
17	24	100.0	147	2	US-09-565-423-4	Sequence 4, Appli
18	24	100.0	148	1	US-07-668-517-2	Sequence 2, Appli
19	24	100.0	148	1	US-07-668-517-15	Sequence 15, Appl
20	24	100.0	149	1	US-07-668-517-3	Sequence 3, Appli
21	24	100.0	149	1	US-07-668-517-16	Sequence 16, Appl
22	24	100.0	150	1	US-07-668-517-4	Sequence 4, Appli
23	24	100.0	150	1	US-07-668-517-5	Sequence 5, Appli
24	24	100.0	150	1	US-07-668-517-6	Sequence 6, Appli
25	24	100.0	150	1	US-07-668-517-8	Sequence 8, Appli
26	24	100.0	150	1	US-07-668-517-9	Sequence 9, Appli
27	24	100.0	150	1	US-07-668-517-10	Sequence 10, Appl
28	24	100.0	150	1	US-07-668-517-11	Sequence 11, Appl
29	24	100.0	150	1	US-07-668-517-12	Sequence 12, Appl
30	24	100.0	150	1	US-07-668-517-13	Sequence 13, Appl
31	24	100.0	150	1	US-07-668-517-14	Sequence 14, Appl
32	24	100.0	150	1	US-07-668-517-17	Sequence 17, Appl
33	24	100.0	150	1	US-07-668-517-29	Sequence 29, Appl
34	24	100.0	150	1	US-07-668-517-31	Sequence 31, Appl
35	24	100.0	150	1	US-07-668-517-35	Sequence 35, Appl
36	24	100.0	150	1	US-07-668-517-37	Sequence 37, Appl
37	24	100.0	150	1	US-07-994-469A-6	Sequence 6, Appli
38	24	100.0	150	1	US-07-994-469A-7	Sequence 7, Appli
39	24	100.0	150	1	US-07-994-469A-8	Sequence 8, Appli
40	24	100.0	150	1	US-07-994-469A-57	Sequence 57, Appl
41	24	100.0	150	2	US-09-286-529-25	Sequence 25, Appl
42	24	100.0	151	1	US-07-668-517-7	Sequence 7, Appli
43	24	100.0	151	1	US-07-668-517-18	Sequence 18, Appl
44	24	100.0	151	1	US-07-668-517-19	Sequence 19, Appl
45	24	100.0	151	1	US-07-668-517-20	Sequence 20, Appl

ALIGNMENTS

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RESULT 1
US-08-107-235-9
; Sequence 9, Application US/08107235
; Patent No. 5587457
;  GENERAL INFORMATION:
;    APPLICANT:  Rathjen, Deborah A
;    APPLICANT:  Ferrante, Antonio
;    APPLICANT:  Widmer, Fred
;    TITLE OF INVENTION:  Neutrophil Stimulating Peptides
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 S. Wacker Dr.
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/107,235
;      FILING DATE:  16-AUG-1993
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/930,415
;      FILING DATE:  12-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDonnell, John J
;      REGISTRATION NUMBER:  26,949
;      REFERENCE/DOCKET NUMBER:  92,622A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..19
;      OTHER INFORMATION:  /note= "PEPTIDE 307 (22-40)"
US-08-107-235-9

  Query Match             100.0%;  Score 24;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 24;
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  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db          8 LNRRA 12


RESULT 2
US-08-178-268-43
; Sequence 43, Application US/08178268
; Patent No. 5795859
;  GENERAL INFORMATION:
;    APPLICANT:  RATHGEN, Deborah A
;    APPLICANT:  WIDMER, Fred
;    APPLICANT:  GRIGG, Geoffrey W
;    APPLICANT:  MACK, Philip O
;    TITLE OF INVENTION:  Peptide which Abrogates TNF and/or LPS Toxicity
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon & Vanderhye P.C.
;      STREET:  1100 No. 5795859th Glebe Road, 8th Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22201-4714
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/178,268
;      FILING DATE:  05-JAN-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MITCHARD, Leonard C
;      REGISTRATION NUMBER:  29,009
;      REFERENCE/DOCKET NUMBER:  47-45
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 816-4000
;      TELEFAX:  (703) 816-4100
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  both
;    MOLECULE TYPE:  peptide
US-08-178-268-43

  Query Match             100.0%;  Score 24;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db          8 LNRRA 12


RESULT 3
US-08-714-960B-9
; Sequence 9, Application US/08714960B
; Patent No. 6121237
;  GENERAL INFORMATION:
;    APPLICANT:  RATHJEN, Deborah A
;    APPLICANT:  FERRANTE, Antonio
;    TITLE OF INVENTION:  Neutrophil Stimulating Peptides
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER & WITCOFF, LTD.
;      STREET:  10 S. Wacker Drive, Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  1.44 Mb storage diskette, 3.50 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  IBM compatible PC/MS-DOS
;      SOFTWARE:  WordPerfect version 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/714,960B
;      FILING DATE:  17-SEP-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PJ9065
;      FILING DATE:  12-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/AU91/00086
;      FILING DATE:  12-MAR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/930,415
;      FILING DATE:  09-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/107,235
;      FILING DATE:  16-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Resis, Robert H.
;      REGISTRATION NUMBER:  32,168
;      REFERENCE/DOCKET NUMBER:  92,622-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 715-1000
;      TELEFAX:  (312) 715-1234
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..19
;      OTHER INFORMATION:  /note= "PEPTIDE 307 (22-40)"
US-08-714-960B-9

  Query Match             100.0%;  Score 24;  DB 2;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db          8 LNRRA 12


RESULT 4
US-09-598-784-9
; Sequence 9, Application US/09598784
; Patent No. 6375928
;  GENERAL INFORMATION:
;       APPLICANT: RATHJEN, Deborah A
;                  FERRANTE, Antonio
;       TITLE OF INVENTION: Neutrophil Stimulating Peptides
;       NUMBER OF SEQUENCES: 19
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BANNER & WITCOFF, LTD.
;            STREET: 10 S. Wacker Drive, Suite 3000
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60606
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: IBM compatible PC/MS-DOS
;            SOFTWARE: WordPerfect version 6.1
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;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/598,784
;              FILING DATE: 21-Jun-2000
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: AU PJ9065
;              FILING DATE: 12-MAR-1990
;              APPLICATION NUMBER: PCT/AU91/00086
;              FILING DATE: 12-MAR-1991
;              APPLICATION NUMBER: US 07/930,415
;              FILING DATE: 09-NOV-1992
;              APPLICATION NUMBER: US 08/107,235
;              FILING DATE: 16-AUG-1993
;              APPLICATION NUMBER: US 08/714,960
;              FILING DATE: 17-SEP-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Resis, Robert H.
;              REGISTRATION NUMBER: 32,168
;              REFERENCE/DOCKET NUMBER: 11341.00001
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (312) 715-1000
;              TELEFAX: (312) 715-1234
;    INFORMATION FOR SEQ ID NO: 9:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 19 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: not relevant
;         MOLECULE TYPE: peptide
;         FEATURE:
;              NAME/KEY:  Peptide
;              LOCATION:  1..19
;              OTHER INFORMATION:  /note= "PEPTIDE 307 (22-40)"
;         SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-598-784-9

  Query Match             100.0%;  Score 24;  DB 2;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db          8 LNRRA 12


RESULT 5
US-09-369-494-16
; Sequence 16, Application US/09369494
; Patent No. 6180607
; GENERAL INFORMATION:
;  APPLICANT: Davies, Christopher
;  APPLICANT: Chen, Dadong
;  APPLICANT: Roczniak, Steve
;  TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
;  FILE REFERENCE: MSB-7260
;  CURRENT APPLICATION NUMBER: US/09/369,494
;  CURRENT FILING DATE: 1999-08-05
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 51
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:fragment from
;   OTHER INFORMATION: computer database
US-09-369-494-16

  Query Match             100.0%;  Score 24;  DB 2;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         19 LNRRA 23


RESULT 6
US-09-358-569D-14
; Sequence 14, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
;  APPLICANT:  Delaria, Kathy
;  APPLICANT:  Roczniak, Steve
;  APPLICANT:  Davies, Christopher
;  TITLE OF INVENTION:  Protein Having Proteinase Inhibitor Activity
;  FILE REFERENCE:  MSB-7259
;  CURRENT APPLICATION NUMBER: US/09/358,569D
;  CURRENT FILING DATE:  1999-07-20
;  NUMBER OF SEQ ID NOS:  15
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 51
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:from computer
;   OTHER INFORMATION: database
US-09-358-569D-14

  Query Match             100.0%;  Score 24;  DB 2;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         19 LNRRA 23


RESULT 7
US-09-569-670-16
; Sequence 16, Application US/09569670
; Patent No. 6689582
; GENERAL INFORMATION:
;  APPLICANT:  Davies, Christopher
;  APPLICANT:  Chen, Dadong
;  APPLICANT:  Roczniak, Steve
;  TITLE OF INVENTION:  Protein Having Proteinase Inhibitor Activity
;  FILE REFERENCE:  MSB-7260
;  CURRENT APPLICATION NUMBER: US/09/569,670
;  CURRENT FILING DATE:  2000-05-12
;  NUMBER OF SEQ ID NOS:  17
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 51
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:fragment from
;   OTHER INFORMATION: computer database
US-09-569-670-16

  Query Match             100.0%;  Score 24;  DB 2;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         19 LNRRA 23


RESULT 8
US-09-513-999C-5811
; Sequence 5811, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
```

```
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 5811
;   LENGTH: 69
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 48
;   OTHER INFORMATION: Xaa= *  or Leu or Ser or Trp
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 56
;   OTHER INFORMATION: Xaa=Ser or Thr
US-09-513-999C-5811

  Query Match             100.0%;  Score 24;  DB 2;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         35 LNRRA 39


RESULT 9
US-09-632-287A-20
; Sequence 20, Application US/09632287A
; Patent No. 6521422
; GENERAL INFORMATION:
;  APPLICANT:  Hsu, Hailing
;  APPLICANT:  Wooden, Scott K
;  APPLICANT:  Boyle, William J
;  TITLE OF INVENTION:  Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
;  FILE REFERENCE:  01017/35550A
;  CURRENT APPLICATION NUMBER: US/09/632,287A
;  CURRENT FILING DATE:  2000-08-03
;  PRIOR APPLICATION NUMBER:  US 60/147,294
;  PRIOR FILING DATE:  1999-08-04
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 71
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-632-287A-20

  Query Match             100.0%;  Score 24;  DB 2;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 93;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         24 LNRRA 28


RESULT 10
US-10-286-696-20
; Sequence 20, Application US/10286696
; Patent No. 6852839
; GENERAL INFORMATION:
;  APPLICANT: Hsu, Hailing
;  APPLICANT:  Wooden, Scott K
;  APPLICANT:  Boyle, William J
;  TITLE OF INVENTION: Fhm, A No. 6852839el Member of the TNF Ligand Supergene Family
;  FILE REFERENCE: 01017/35550A
;  CURRENT APPLICATION NUMBER: US/10/286,696
;  CURRENT FILING DATE:  2002-11-01
;  PRIOR APPLICATION NUMBER: US 60/147,294
;  PRIOR FILING DATE: 1999-08-04
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 71
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-286-696-20

  Query Match             100.0%;  Score 24;  DB 2;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 93;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         24 LNRRA 28


RESULT 11
US-09-314-268-133
; Sequence 133, Application US/09314268
; Patent No. 6346377
; GENERAL INFORMATION:
;  APPLICANT: Doorbar, John
;  TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA
;  TITLE OF INVENTION: VIRUSES
;  FILE REFERENCE: 3789/80902
;  CURRENT APPLICATION NUMBER: US/09/314,268
;  CURRENT FILING DATE: 1999-03-19
;  EARLIER APPLICATION NUMBER: 09/314,268
;  EARLIER FILING DATE: 1999-05-18
;  NUMBER OF SEQ ID NOS: 179
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
;   LENGTH: 99
;   TYPE: PRT
;   ORGANISM: Human papillomavirus type 20
US-09-314-268-133

  Query Match             100.0%;  Score 24;  DB 2;  Length 99;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         46 LNRRA 50


RESULT 12
US-09-911-777-5
; Sequence 5, Application US/09911777
; Patent No. 6869605
; GENERAL INFORMATION:
;  APPLICANT: BIOGEN, INC.
;  APPLICANT:  APOTECH S.A.
;  APPLICANT:  BROWNING, Jeffrey
;  APPLICANT:  AMBROSE, Christine
;  APPLICANT:  MACKAY, Fabienne
;  APPLICANT:  TSCHOPP, Jurg
;  APPLICANT:  SCHNEIDER, Pascal
;  TITLE OF INVENTION: BAFF, Inhibitors Thereof and Their Use
;  TITLE OF INVENTION:  in the Modulation of B-Cell Response
;  FILE REFERENCE: A070 US
;  CURRENT APPLICATION NUMBER: US/09/911,777
;  CURRENT FILING DATE:  2001-07-24
;  PRIOR APPLICATION NUMBER: 60/117,169
;  PRIOR FILING DATE: 1999-01-25
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;  PRIOR APPLICATION NUMBER: 60/143,228
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: PCT/US00/01788
;  PRIOR FILING DATE: 2000-01-25
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 104
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-911-777-5

  Query Match             100.0%;  Score 24;  DB 2;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         21 LNRRA 25


RESULT 13
US-07-994-469A-10
; Sequence 10, Application US/07994469A
; Patent No. 5519119
;  GENERAL INFORMATION:
;    APPLICANT:  Yamada, No. 5519119utoshi
;    APPLICANT:  Kato, Masanari
;    APPLICANT:  Miyata, Keizo
;    APPLICANT:  Aoyama, Yoshiyuki
;    APPLICANT:  Shikama, Hiroshi
;    TITLE OF INVENTION:  Polypeptide
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 Jefferson Davis Highway, Fourth Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/994,469A
;      FILING DATE:  21-DEC-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5519119man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  72-085-0 FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)413-3000
;      TELEFAX:  (703)413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  139 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-994-469A-10

  Query Match             100.0%;  Score 24;  DB 1;  Length 139;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
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Db         19 LNRRA 23


RESULT 14
US-07-994-469A-9
; Sequence 9, Application US/07994469A
; Patent No. 5519119
;  GENERAL INFORMATION:
;    APPLICANT:  Yamada, No. 5519119utoshi
;    APPLICANT:  Kato, Masanari
;    APPLICANT:  Miyata, Keizo
;    APPLICANT:  Aoyama, Yoshiyuki
;    APPLICANT:  Shikama, Hiroshi
;    TITLE OF INVENTION:  Polypeptide
;    NUMBER OF SEQUENCES:  101
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 Jefferson Davis Highway, Fourth Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/994,469A
;      FILING DATE:  21-DEC-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5519119man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  72-085-0 FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)413-3000
;      TELEFAX:  (703)413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  145 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-994-469A-9

  Query Match             100.0%;  Score 24;  DB 1;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         25 LNRRA 29


RESULT 15
US-07-668-517-1
; Sequence 1, Application US/07668517
; Patent No. 5262309
;  GENERAL INFORMATION:
;    APPLICANT:  Satoshi NAKAMURA et al.
;    TITLE OF INVENTION:  No. 5262309el Physiologically Active
;    TITLE OF INVENTION:  Polypeptide, Recombinant Plasmid, Recombinant Microorganism
;    TITLE OF INVENTION:  Cell, Pharmaceutical Composition and Method of Recovering
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 500 Kb
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;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  DisplayWrite
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/668,517
;      FILING DATE:  19910322
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Matthew Jacob
;      REGISTRATION NUMBER:  25,154
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:  202-371-8856
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  147 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
US-07-668-517-1

  Query Match             100.0%;  Score 24;  DB 1;  Length 147;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         19 LNRRA 23


Search completed: January 12, 2006, 16:20:05
Job time : 19 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 12, 2006, 16:19:26 ; Search time 15.5 Seconds
(without alignments)
3.050 Million cell updates/sec

Title: US-10-716-030-1
Perfect score: 24
Sequence: 1 LNRRA 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	100.0	102	6	US-10-689-742-21	Sequence 21, Appl
2	24	100.0	104	7	US-11-065-669-5	Sequence 5, Appli
3	24	100.0	157	7	US-11-010-954-1	Sequence 1, Appli
4	24	100.0	157	7	US-11-053-750-1	Sequence 1, Appli
5	24	100.0	157	7	US-11-053-749-1	Sequence 1, Appli
6	24	100.0	157	7	US-11-108-001-12	Sequence 12, Appl
7	24	100.0	158	7	US-11-082-544-4	Sequence 4, Appli
8	24	100.0	164	7	US-11-108-001-2	Sequence 2, Appli
9	24	100.0	180	7	US-11-082-544-8	Sequence 8, Appli
10	24	100.0	399	7	US-11-065-943-53	Sequence 53, Appl
11	24	100.0	401	7	US-11-055-822-336	Sequence 336, App
12	24	100.0	421	7	US-11-120-308-64	Sequence 64, Appl
13	24	100.0	440	7	US-11-102-240-134	Sequence 134, App
14	22	91.7	164	6	US-10-467-657-9140	Sequence 9140, Ap
15	22	91.7	229	6	US-10-467-657-916	Sequence 916, App
16	22	91.7	378	6	US-10-467-657-1796	Sequence 1796, Ap
17	22	91.7	547	7	US-11-156-003-16	Sequence 16, Appl
18	22	91.7	1827	7	US-11-057-058-62	Sequence 62, Appl
19	21	87.5	295	6	US-10-467-657-620	Sequence 620, App
20	21	87.5	311	6	US-10-873-528-117	Sequence 117, App
21	21	87.5	322	6	US-10-689-742-46	Sequence 46, Appl
22	21	87.5	322	6	US-10-821-234-891	Sequence 891, App
23	21	87.5	347	6	US-10-821-234-1379	Sequence 1379, Ap
24	21	87.5	350	6	US-10-467-657-1972	Sequence 1972, Ap
25	21	87.5	409	7	US-11-113-424-73	Sequence 73, Appl
26	21	87.5	449	6	US-10-763-712A-83	Sequence 83, Appl
27	21	87.5	478	6	US-10-793-626-1348	Sequence 1348, Ap
28	21	87.5	503	7	US-11-113-424-72	Sequence 72, Appl
29	21	87.5	559	6	US-10-821-234-1513	Sequence 1513, Ap
30	21	87.5	570	7	US-11-113-424-69	Sequence 69, Appl
31	21	87.5	570	7	US-11-113-424-71	Sequence 71, Appl
32	21	87.5	620	7	US-11-113-424-70	Sequence 70, Appl
33	21	87.5	676	6	US-10-510-947-1	Sequence 1, Appli
34	21	87.5	720	7	US-11-113-424-28	Sequence 28, Appl
35	21	87.5	747	7	US-11-113-424-26	Sequence 26, Appl
36	21	87.5	756	6	US-10-467-657-8694	Sequence 8694, Ap
37	21	87.5	783	7	US-11-082-389-354	Sequence 354, App
38	21	87.5	1368	6	US-10-770-303-2	Sequence 2, Appli
39	21	87.5	1368	7	US-11-185-372-2	Sequence 2, Appli
40	20	83.3	53	6	US-10-467-657-6170	Sequence 6170, Ap
41	20	83.3	60	6	US-10-502-972-13	Sequence 13, Appl
42	20	83.3	60	6	US-10-502-972-17	Sequence 17, Appl
43	20	83.3	60	6	US-10-502-972-19	Sequence 19, Appl
44	20	83.3	61	6	US-10-467-657-1222	Sequence 1222, Ap
45	20	83.3	61	6	US-10-467-657-9027	Sequence 9027, Ap

ALIGNMENTS

RESULT 1
US-10-689-742-21
; Sequence 21, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: LaVallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-21

Query Match 100.0%; Score 24; DB 6; Length 102;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
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Db 84 LNRRA 88

RESULT 2
US-11-065-669-5
; Sequence 5, Application US/11065669
; Publication No. US20050244411A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Kalled, Susan
; TITLE OF INVENTION: BAFF, INHIBITORS THEREOF AND THEIR USE IN THE
; TITLE OF INVENTION: MODULATION OF B-CELL RESPONSE
; FILE REFERENCE: 08201.0024-04000
; CURRENT APPLICATION NUMBER: US/11/065,669
; CURRENT FILING DATE: 2005-02-24

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;  PRIOR APPLICATION NUMBER: 10/045,574
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: 09/911,777
;  PRIOR FILING DATE: 2001-07-24
;  PRIOR APPLICATION NUMBER: 60/143,228
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: PCT/US00/01788
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 60/117,169
;  PRIOR FILING DATE: 1999-01-25
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 104
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-065-669-5

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  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
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Db         21 LNRRA 25


RESULT 3
US-11-010-954-1
; Sequence 1, Application US/11010954
; Publication No. US20050249735A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David
;  APPLICANT:  Siegel, Scott
;  APPLICANT:  Shealy, David
;  TITLE OF INVENTION: Methods of Treating Ankylosing Spondylitis Using Anti-TNF Antibod
;  TITLE OF INVENTION:  and Peptides of Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-043
;  CURRENT APPLICATION NUMBER: US/11/010,954
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: US 10/637,759
;  PRIOR FILING DATE: 2003-08-08
;  PRIOR APPLICATION NUMBER: US 09/920,137
;  PRIOR FILING DATE: 2001-08-01
;  PRIOR APPLICATION NUMBER: US 09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: US 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: US 60/236,826
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: US 60/223,360
;  PRIOR FILING DATE: 2000-08-07
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-010-954-1

  Query Match             100.0%;  Score 24;  DB 7;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         29 LNRRA 33


RESULT 4
US-11-053-750-1
; Sequence 1, Application US/11053750
; Publication No. US20050255104A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David
;  APPLICANT:  Siegel, Scott
;  APPLICANT:  Scallon, Bernard
;  TITLE OF INVENTION: Methods of Treating Psoriasis Using
;  TITLE OF INVENTION:  Anti-TNF Receptor Fusion Proteins
;  FILE REFERENCE: 0975.1005-045
;  CURRENT APPLICATION NUMBER: US/11/053,750
;  CURRENT FILING DATE:  2005-02-07
;  PRIOR APPLICATION NUMBER: U.S. 09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 09/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-053-750-1

  Query Match             100.0%;  Score 24;  DB 7;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         29 LNRRA 33


RESULT 5
US-11-053-749-1
; Sequence 1, Application US/11053749
; Publication No. US20050260201A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David
;  APPLICANT:  Siegel, Scott
;  APPLICANT:  Scallon, Bernard
;  TITLE OF INVENTION: Methods of Treating Rheumatoid Arthritis
;  TITLE OF INVENTION:  Using Anti-TNF Receptor Fusion Proteins
;  FILE REFERENCE: 0975.1005-040
;  CURRENT APPLICATION NUMBER: US/11/053,749
;  CURRENT FILING DATE:  2005-02-07
;  PRIOR APPLICATION NUMBER: US/09/927,703
;  PRIOR FILING DATE: 2001-08-10
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;  PRIOR APPLICATION NUMBER: U.S. 09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S.08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;    LENGTH: 157
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-11-053-749-1

  Query Match             100.0%;  Score 24;  DB 7;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         29 LNRRA 33


RESULT 6
US-11-108-001-12
; Sequence 12, Application US/11108001
; Publication No. US20050265962A1
; GENERAL INFORMATION:
;  APPLICANT: Desjarlais, John R.
;  APPLICANT:  Steed, Paul Michael
;  APPLICANT:  Zalevsky, Jonathan
;  APPLICANT:  Szymkowski, David Edmund
;  TITLE OF INVENTION: PROTEIN BASED TNF-ALPHA VARIANTS FOR THE TREATMENT OF TNF-ALPHA
;  TITLE OF INVENTION:  RELATED DISORDERS
;  FILE REFERENCE: A-68990-7
;  CURRENT APPLICATION NUMBER: US/11/108,001
;  CURRENT FILING DATE:  2005-04-14
;  PRIOR APPLICATION NUMBER: US 10/963,994
;  PRIOR FILING DATE: 2004-10-12
;  PRIOR APPLICATION NUMBER: US 09/798,789
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: US 09/945,150
;  PRIOR FILING DATE: 2001-08-31
;  PRIOR APPLICATION NUMBER: US 09/981,289
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: US 10/262,630
;  PRIOR FILING DATE: 2002-09-30
;  PRIOR APPLICATION NUMBER: US 60/553,908
;  PRIOR FILING DATE: 2004-03-17
;  PRIOR APPLICATION NUMBER: US 60/510,430
;  PRIOR FILING DATE: 2003-10-10
;  PRIOR APPLICATION NUMBER: US 60/509,960
;  PRIOR FILING DATE: 2003-10-09
;  PRIOR APPLICATION NUMBER: US 60/528,275
;  PRIOR FILING DATE: 2003-12-08
;  PRIOR APPLICATION NUMBER: US 60/523,647
;  PRIOR FILING DATE: 2003-11-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;    LENGTH: 157
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-11-108-001-12

  Query Match             100.0%;  Score 24;  DB 7;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         29 LNRRA 33


RESULT 7
US-11-082-544-4
; Sequence 4, Application US/11082544
; Publication No. US20050249706A1
; GENERAL INFORMATION:
;  APPLICANT: Bermudes, G.
;  APPLICANT:  King, I.
;  APPLICANT:  Clairmont, C.
;  APPLICANT:  Lin, S.
;  APPLICANT:  Belcourt, M.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
;  FILE REFERENCE: 8002-059
;  CURRENT APPLICATION NUMBER: US/11/082,544
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: US/09/645,415
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: 60/157,581
;  PRIOR FILING DATE: 1999-10-04
;  PRIOR APPLICATION NUMBER: 60/157,637
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;    LENGTH: 158
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-11-082-544-4

  Query Match             100.0%;  Score 24;  DB 7;  Length 158;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         30 LNRRA 34


RESULT 8
US-11-108-001-2
; Sequence 2, Application US/11108001
; Publication No. US20050265962A1
; GENERAL INFORMATION:
;  APPLICANT: Desjarlais, John R.
;  APPLICANT:  Steed, Paul Michael
;  APPLICANT:  Zalevsky, Jonathan
;  APPLICANT:  Szymkowski, David Edmund
;  TITLE OF INVENTION: PROTEIN BASED TNF-ALPHA VARIANTS FOR THE TREATMENT OF TNF-ALPHA
;  TITLE OF INVENTION:  RELATED DISORDERS
;  FILE REFERENCE: A-68990-7
;  CURRENT APPLICATION NUMBER: US/11/108,001
;  CURRENT FILING DATE:  2005-04-14
;  PRIOR APPLICATION NUMBER: US 10/963,994
;  PRIOR FILING DATE: 2004-10-12
;  PRIOR APPLICATION NUMBER: US 09/798,789
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: US 09/945,150
;  PRIOR FILING DATE: 2001-08-31
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;  PRIOR APPLICATION NUMBER: US 09/981,289
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: US 10/262,630
;  PRIOR FILING DATE: 2002-09-30
;  PRIOR APPLICATION NUMBER: US 60/553,908
;  PRIOR FILING DATE: 2004-03-17
;  PRIOR APPLICATION NUMBER: US 60/510,430
;  PRIOR FILING DATE: 2003-10-10
;  PRIOR APPLICATION NUMBER: US 60/509,960
;  PRIOR FILING DATE: 2003-10-09
;  PRIOR APPLICATION NUMBER: US 60/528,275
;  PRIOR FILING DATE: 2003-12-08
;  PRIOR APPLICATION NUMBER: US 60/523,647
;  PRIOR FILING DATE: 2003-11-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
;   LENGTH: 164
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-108-001-2

  Query Match             100.0%;  Score 24;  DB 7;  Length 164;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         36 LNRRA 40


RESULT 9
US-11-082-544-8
; Sequence 8, Application US/11082544
; Publication No. US20050249706A1
; GENERAL INFORMATION:
;  APPLICANT: Bermudes, G.
;  APPLICANT:  King, I.
;  APPLICANT:  Clairmont, C.
;  APPLICANT:  Lin, S.
;  APPLICANT:  Belcourt, M.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
;  FILE REFERENCE: 8002-059
;  CURRENT APPLICATION NUMBER: US/11/082,544
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: US/09/645,415
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: 60/157,581
;  PRIOR FILING DATE: 1999-10-04
;  PRIOR APPLICATION NUMBER: 60/157,637
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion construct
US-11-082-544-8

  Query Match             100.0%;  Score 24;  DB 7;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         52 LNRRA 56


RESULT 10
US-11-065-943-53
; Sequence 53, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
;  APPLICANT: JESTIN, JEAN-LUC
;  APPLICANT:  VICHIER-GUERRE, SOPHIE
;  APPLICANT:  FERRIS, STEPHANE
;  TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
;  TITLE OF INVENTION:  VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
;  TITLE OF INVENTION:  METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
;  FILE REFERENCE: 266426US0XCIP
;  CURRENT APPLICATION NUMBER: US/11/065,943
;  CURRENT FILING DATE:  2005-02-25
;  PRIOR APPLICATION NUMBER: US 10/787,219
;  PRIOR FILING DATE: 2004-02-27
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 53
;   LENGTH: 399
;   TYPE: PRT
;   ORGANISM: Bordetella pertussis
US-11-065-943-53

  Query Match             100.0%;  Score 24;  DB 7;  Length 399;
  Best Local Similarity   100.0%;  Pred. No. 62;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db        283 LNRRA 287


RESULT 11
US-11-055-822-336
; Sequence 336, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Markus
;  APPLICANT:  Kroger, Burkhard
;  APPLICANT:  Schroder, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
;  TITLE OF INVENTION:  METABOLIC PATHWAY PROTEINS
;  FILE REFERENCE: BGI-121CPCN
;  CURRENT APPLICATION NUMBER: US/11/055,822
;  CURRENT FILING DATE:  2005-02-11
;  PRIOR APPLICATION NUMBER: 09/606,740
;  PRIOR FILING DATE: 2000-06-23
;  PRIOR APPLICATION NUMBER: 60/141,031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: 60/142,101
;  PRIOR FILING DATE: 1999-07-02
;  PRIOR APPLICATION NUMBER: 60/148,613
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 60/187,970
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: DE 19930476.9
;  PRIOR FILING DATE: 1999-07-01
;  PRIOR APPLICATION NUMBER: DE 19931415.2
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931418.7
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931419.5
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931420.9
;  PRIOR FILING DATE: 1999-07-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 336
;   LENGTH: 401
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
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US-11-055-822-336

Query Match 100.0%; Score 24; DB 7; Length 401;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 243 LNRRA 247

RESULT 12
US-11-120-308-64
; Sequence 64, Application US/11120308
; Publication No. US20060005277A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Forge, Charlie
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: cDNAS Encoding Polypeptides
; FILE REFERENCE: BB-1365 US NA
; CURRENT APPLICATION NUMBER: US/11/120,308
; CURRENT FILING DATE: 2005-05-02
; PRIOR APPLICATION NUMBER: US/10/078,770
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/614,188
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,400
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/153,534
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/161,223
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/159,878
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/157,401
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/143,419
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,409
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 64
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Zea mays
US-11-120-308-64

Query Match 100.0%; Score 24; DB 7; Length 421;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 185 LNRRA 189

RESULT 13
US-11-102-240-134
; Sequence 134, Application US/11102240
; Publication No. US20050260647A1
; GENERAL INFORMATION:
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS
; TITLE OF INVENTION: ESOPHAGEAL TUMOR
; FILE REFERENCE: P3230R1C106C
; CURRENT APPLICATION NUMBER: US/11/102,240
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 10/063662
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 199-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 134
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-102-240-134

Query Match 100.0%; Score 24; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 272 LNRRA 276

RESULT 14
US-10-467-657-9140
; Sequence 9140, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9140
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9140

Query Match 91.7%; Score 22; DB 6; Length 164;
Best Local Similarity 80.0%; Pred. No. 76;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
:||||
Db 13 INRRA 17

RESULT 15
US-10-467-657-916
; Sequence 916, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12

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;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 916
;   LENGTH: 229
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-916

  Query Match             91.7%;  Score 22;  DB 6;  Length 229;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              :||||
Db         18 INRRA 22


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Job time : 15.5 secs
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OM protein - protein search, using sw model

Run on: January 12, 2006, 16:18:51 ; Search time 86 Seconds
(without alignments)
24.292 Million cell updates/sec

Title: US-10-716-030-1
Perfect score: 24
Sequence: 1 LNRRA 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	100.0	7	4	US-10-405-339-40	Sequence 40, Appl
2	24	100.0	11	4	US-10-617-876-29	Sequence 29, Appl
3	24	100.0	14	4	US-10-617-876-102	Sequence 102, App
4	24	100.0	17	4	US-10-272-411-47	Sequence 47, Appl
5	24	100.0	17	4	US-10-272-328A-47	Sequence 47, Appl
6	24	100.0	19	4	US-10-119-621-9	Sequence 9, Appli
7	24	100.0	19	4	US-10-264-844-9	Sequence 9, Appli
8	24	100.0	19	4	US-10-265-344-9	Sequence 9, Appli
9	24	100.0	19	4	US-10-265-451-9	Sequence 9, Appli
10	24	100.0	19	4	US-10-264-844-9	Sequence 9, Appli
11	24	100.0	32	4	US-10-029-386-32371	Sequence 32371, A
12	24	100.0	36	4	US-10-050-704-222	Sequence 222, App
13	24	100.0	36	4	US-10-798-512-222	Sequence 222, App
14	24	100.0	51	4	US-10-275-589-11	Sequence 11, Appl
15	24	100.0	51	4	US-10-019-065A-2	Sequence 2, Appli
16	24	100.0	51	4	US-10-437-963-131854	Sequence 131854,
17	24	100.0	51	5	US-10-874-850-2	Sequence 2, Appli
18	24	100.0	52	4	US-10-449-831A-234	Sequence 234, App
19	24	100.0	62	4	US-10-425-115-331778	Sequence 331778,
20	24	100.0	63	4	US-10-425-115-366584	Sequence 366584,
21	24	100.0	70	3	US-09-864-408A-7076	Sequence 7076, Ap
22	24	100.0	71	4	US-10-286-696-20	Sequence 20, Appl
23	24	100.0	71	5	US-10-890-368-20	Sequence 20, Appl
24	24	100.0	71	5	US-10-889-948-20	Sequence 20, Appl
25	24	100.0	73	4	US-10-437-963-188160	Sequence 188160,
26	24	100.0	73	4	US-10-425-115-201422	Sequence 201422,
27	24	100.0	74	4	US-10-767-701-62884	Sequence 62884, A
28	24	100.0	80	4	US-10-425-114-41490	Sequence 41490, A
29	24	100.0	80	4	US-10-425-115-291629	Sequence 291629,
30	24	100.0	82	4	US-10-319-799-72	Sequence 72, Appl
31	24	100.0	84	4	US-10-425-115-295879	Sequence 295879,
32	24	100.0	87	3	US-09-864-408A-7852	Sequence 7852, Ap
33	24	100.0	92	4	US-10-050-704-226	Sequence 226, App
34	24	100.0	92	4	US-10-798-512-226	Sequence 226, App
35	24	100.0	94	4	US-10-425-115-307564	Sequence 307564,
36	24	100.0	95	4	US-10-437-963-173068	Sequence 173068,
37	24	100.0	99	4	US-10-008-524A-133	Sequence 133, App
38	24	100.0	99	4	US-10-350-719-133	Sequence 133, App
39	24	100.0	100	4	US-10-437-963-137984	Sequence 137984,
40	24	100.0	100	4	US-10-425-115-271761	Sequence 271761,
41	24	100.0	102	3	US-09-746-783-21	Sequence 21, Appl
42	24	100.0	104	3	US-09-911-777-5	Sequence 5, Appli
43	24	100.0	104	4	US-10-045-574A-5	Sequence 5, Appli
44	24	100.0	104	6	US-11-016-922-5	Sequence 5, Appli
45	24	100.0	104	6	US-11-080-973-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-405-339-40
; Sequence 40, Application US/10405339
; Publication No. US20030190364A1
; GENERAL INFORMATION:
; APPLICANT: Panitch, Alyssa
; APPLICANT: Seal, Brandon
; TITLE OF INVENTION: Biological Affinity Based Delivery Systems
; FILE REFERENCE: 9138-0079US
; CURRENT APPLICATION NUMBER: US/10/405,339
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US 60/369,568
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-405-339-40

Query Match 100.0%; Score 24; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
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Db 1 LNRRA 5

RESULT 2
US-10-617-876-29
; Sequence 29, Application US/10617876
; Publication No. US20040076611A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Tissot, Alain
; APPLICANT: Pumpens, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Molecular Antigen Arrays
; FILE REFERENCE: 1700.0310001
; CURRENT APPLICATION NUMBER: US/10/617,876
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/396,126
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-876-29

Query Match 100.0%; Score 24; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 5 LNRRA 9

RESULT 3
US-10-617-876-102
; Sequence 102, Application US/10617876
; Publication No. US20040076611A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Tissot, Alain
; APPLICANT: Pumpens, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Molecular Antigen Arrays
; FILE REFERENCE: 1700.0310001
; CURRENT APPLICATION NUMBER: US/10/617,876
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/396,126
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 102
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C-TNF-a mutant
US-10-617-876-102

Query Match 100.0%; Score 24; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 8 LNRRA 12

RESULT 4
US-10-272-411-47
; Sequence 47, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272,411
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-411-47

Query Match 100.0%; Score 24; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 11 LNRRA 15

RESULT 5
US-10-272-328A-47
; Sequence 47, Application US/10272328A
; Publication No. US20030109444A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-328A-47

Query Match 100.0%; Score 24; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 11 LNRRA 15

RESULT 6
US-10-119-621-9
; Sequence 9, Application US/10119621
; Publication No. US20030064021A1
; GENERAL INFORMATION:
; APPLICANT: RATHJEN, Deborah A
; FERRANTE, Antonio
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: IBM compatible PC/MS-DOS
; SOFTWARE: WordPerfect version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/119,621
; FILING DATE: 10-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/598,784
; FILING DATE: 21-Jun-2000
; APPLICATION NUMBER: AU PJ9065
; FILING DATE: 12-MAR-1990
; APPLICATION NUMBER: PCT/AU91/00086
; FILING DATE: 12-MAR-1991

```
;              APPLICATION NUMBER: US 07/930,415
;              FILING DATE: 09-NOV-1992
;              APPLICATION NUMBER: US 08/107,235
;              FILING DATE: 16-AUG-1993
;              APPLICATION NUMBER: US 08/714,960
;              FILING DATE: 17-SEP-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Resis, Robert H.
;              REGISTRATION NUMBER: 32,168
;              REFERENCE/DOCKET NUMBER: 11341.00001
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (312) 715-1000
;              TELEFAX: (312) 715-1234
;    INFORMATION FOR SEQ ID NO: 9:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 19 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: not relevant
;         MOLECULE TYPE: peptide
;         FEATURE:
;              NAME/KEY:  Peptide
;              LOCATION:  1..19
;              OTHER INFORMATION:  /note= "PEPTIDE 307 (22-40)"
;         SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-119-621-9

  Query Match             100.0%;  Score 24;  DB 4;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db          8 LNRRA 12


RESULT 7
US-10-264-844-9
; Sequence 9, Application US/10264844
; Publication No. US20030139577A1
; GENERAL INFORMATION:
;  APPLICANT: Rathjen, Deborah Ann
;  APPLICANT:  Aston, Roger
;  TITLE OF INVENTION: TUMOUR NECROSIS FACTOR BINDING LIGANDS
;  FILE REFERENCE: 273402002309
;  CURRENT APPLICATION NUMBER: US/10/264,844
;  CURRENT FILING DATE:  2002-10-03
;  PRIOR APPLICATION NUMBER: US 09/736,630
;  PRIOR FILING DATE: 2000-12-13
;  PRIOR APPLICATION NUMBER: US 09/364,039
;  PRIOR FILING DATE: 1999-07-30
;  PRIOR APPLICATION NUMBER: US 08/823,893
;  PRIOR FILING DATE: 1997-03-17
;  PRIOR APPLICATION NUMBER: US 08/344,133
;  PRIOR FILING DATE: 1994-11-23
;  PRIOR APPLICATION NUMBER: US 07/828,956
;  PRIOR FILING DATE: 1992-02-18
;  PRIOR APPLICATION NUMBER: PCT/AU90/00337
;  PRIOR FILING DATE: 1990-08-07
;  PRIOR APPLICATION NUMBER: AU PJ7576
;  PRIOR FILING DATE: 1989-11-24
;  PRIOR APPLICATION NUMBER: AU PJ5662
;  PRIOR FILING DATE: 1989-08-07
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct of amino acid residues 22-40
;   OTHER INFORMATION: from sequence of mature human tumor necrosis
;   OTHER INFORMATION: factor alpha
US-10-264-844-9

  Query Match             100.0%;  Score 24;  DB 4;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db          8 LNRRA 12


RESULT 8
US-10-265-344-9
; Sequence 9, Application US/10265344
; Publication No. US20030139580A1
; GENERAL INFORMATION:
;  APPLICANT: Rathjen, Deborah Ann
;  APPLICANT:  Aston, Roger
;  TITLE OF INVENTION: TUMOUR NECROSIS FACTOR BINDING LIGANDS
;  FILE REFERENCE: 273402502301
;  CURRENT APPLICATION NUMBER: US/10/265,344
;  CURRENT FILING DATE:  2002-10-03
;  PRIOR APPLICATION NUMBER: US 09/736,630
;  PRIOR FILING DATE: 2000-12-13
;  PRIOR APPLICATION NUMBER: US 09/364,039
;  PRIOR FILING DATE: 1999-07-30
;  PRIOR APPLICATION NUMBER: US 08/823,893
;  PRIOR FILING DATE: 1997-03-17
;  PRIOR APPLICATION NUMBER: US 08/344,133
;  PRIOR FILING DATE: 1994-11-23
;  PRIOR APPLICATION NUMBER: US 07/828,956
;  PRIOR FILING DATE: 1992-02-18
;  PRIOR APPLICATION NUMBER: PCT/AU90/00337
;  PRIOR FILING DATE: 1990-08-07
;  PRIOR APPLICATION NUMBER: AU PJ7576
;  PRIOR FILING DATE: 1989-11-24
;  PRIOR APPLICATION NUMBER: AU PJ5662
;  PRIOR FILING DATE: 1989-08-07
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct of amino acid residues 22-40
;   OTHER INFORMATION: from sequence of mature human tumor necrosis
;   OTHER INFORMATION: factor alpha
US-10-265-344-9

  Query Match             100.0%;  Score 24;  DB 4;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db          8 LNRRA 12


RESULT 9
US-10-265-451-9
; Sequence 9, Application US/10265451
; Publication No. US20030162948A1
; GENERAL INFORMATION:
;  APPLICANT: Rathjen, Deborah Ann
;  APPLICANT:  Aston, Roger
;  TITLE OF INVENTION: TUMOUR NECROSIS FACTOR BINDING LIGANDS
;  FILE REFERENCE: 273402002308
;  CURRENT APPLICATION NUMBER: US/10/265,451
;  CURRENT FILING DATE:  2002-10-03
;  PRIOR APPLICATION NUMBER: US 09/736,630
;  PRIOR FILING DATE: 2000-12-13
;  PRIOR APPLICATION NUMBER: US 09/364,039
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;  PRIOR FILING DATE: 1999-07-30
;  PRIOR APPLICATION NUMBER: US 08/823,893
;  PRIOR FILING DATE: 1997-03-17
;  PRIOR APPLICATION NUMBER: US 08/344,133
;  PRIOR FILING DATE: 1994-11-23
;  PRIOR APPLICATION NUMBER: US 07/828,956
;  PRIOR FILING DATE: 1992-02-18
;  PRIOR APPLICATION NUMBER: PCT/AU90/00337
;  PRIOR FILING DATE: 1999-08-07
;  PRIOR APPLICATION NUMBER: AU PJ7576
;  PRIOR FILING DATE: 1989-11-24
;  PRIOR APPLICATION NUMBER: AU PJ5662
;  PRIOR FILING DATE: 1989-08-07
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct of amino acid residues 22-40
;   OTHER INFORMATION: from sequence of mature human tumor necrosis
;   OTHER INFORMATION: factor alpha
US-10-265-451-9

  Query Match             100.0%;  Score 24;  DB 4;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db          8 LNRRA 12


RESULT 10
US-10-264-844-9
; Sequence 9, Application US/10264844
; Publication No. US20040214993A2
; GENERAL INFORMATION:
;  APPLICANT: Rathjen, Deborah Ann
;  APPLICANT:  Aston, Roger
;  TITLE OF INVENTION: TUMOUR NECROSIS FACTOR BINDING LIGANDS
;  FILE REFERENCE: 273402002309
;  CURRENT APPLICATION NUMBER: US/10/264,844
;  CURRENT FILING DATE:  2002-10-03
;  PRIOR APPLICATION NUMBER: US 09/736,630
;  PRIOR FILING DATE: 2000-12-13
;  PRIOR APPLICATION NUMBER: US 09/364,039
;  PRIOR FILING DATE: 1999-07-30
;  PRIOR APPLICATION NUMBER: US 08/823,893
;  PRIOR FILING DATE: 1997-03-17
;  PRIOR APPLICATION NUMBER: US 08/344,133
;  PRIOR FILING DATE: 1994-11-23
;  PRIOR APPLICATION NUMBER: US 07/828,956
;  PRIOR FILING DATE: 1992-02-18
;  PRIOR APPLICATION NUMBER: PCT/AU90/00337
;  PRIOR FILING DATE: 1990-08-07
;  PRIOR APPLICATION NUMBER: AU PJ7576
;  PRIOR FILING DATE: 1989-11-24
;  PRIOR APPLICATION NUMBER: AU PJ5662
;  PRIOR FILING DATE: 1989-08-07
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct of amino acid residues 22-40
;   OTHER INFORMATION: from sequence of mature human tumor necrosis
;   OTHER INFORMATION: factor alpha
US-10-264-844-9

  Query Match             100.0%;  Score 24;  DB 4;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 97;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db          8 LNRRA 12


RESULT 11
US-10-029-386-32371
; Sequence 32371, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32371
;   LENGTH: 32
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL117187.3
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL =   2
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.5
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL =   3
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
US-10-029-386-32371

  Query Match             100.0%;  Score 24;  DB 4;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         24 LNRRA 28


RESULT 12
US-10-050-704-222
; Sequence 222, Application US/10050704
; Publication No. US20030050442A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 62 Human Secreted Proteins
;  FILE REFERENCE: PZ039P1
;  CURRENT APPLICATION NUMBER: US/10/050,704
;  CURRENT FILING DATE:  2002-01-18
;  PRIOR APPLICATION NUMBER: 09/684,524
;  PRIOR FILING DATE: 2000-10-10
;  PRIOR APPLICATION NUMBER: PCT/US00/08979
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/128,693
;  PRIOR FILING DATE: 1999-04-09
;  PRIOR APPLICATION NUMBER: 60/130,991
;  PRIOR FILING DATE: 1999-04-26
;  NUMBER OF SEQ ID NOS: 344
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 222
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-10-050-704-222

Query Match 100.0%; Score 24; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
||||||
Db 30 LNRRA 34

RESULT 13
US-10-798-512-222
; Sequence 222, Application US/10798512
; Publication No. US20040152164A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: PZ039P1
; CURRENT APPLICATION NUMBER: US/10/798,512
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US/09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 222
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-798-512-222

Query Match 100.0%; Score 24; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
||||||
Db 30 LNRRA 34

RESULT 14
US-10-275-589-11
; Sequence 11, Application US/10275589
; Publication No. US20040023864A1
; GENERAL INFORMATION:
; APPLICANT: Dubois-Stringfellow, Nathalie
; APPLICANT: Steve, Roczniak
; APPLICANT: Zolotorev, Alya
; TITLE OF INVENTION: Method of Regulating Angiogenesis Using RYK Protein
; FILE REFERENCE: MSB 7266
; CURRENT APPLICATION NUMBER: US/10/275,589
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 09/568,783
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 51
; TYPE: PRT
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: Illustrative random sequence
US-10-275-589-11

Query Match 100.0%; Score 24; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
||||||
Db 19 LNRRA 23

RESULT 15
US-10-019-065A-2
; Sequence 2, Application US/10019065A
; Publication No. US20040086501A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Corporation
; TITLE OF INVENTION: Protein Having Activity As An Angiogenesis Modulator
; FILE REFERENCE: MSB-7265-PCT
; CURRENT APPLICATION NUMBER: US/10/019,065A
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/266,300
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Random sequence
US-10-019-065A-2

Query Match 100.0%; Score 24; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
||||||
Db 19 LNRRA 23

Search completed: January 12, 2006, 16:34:38
Job time : 87 secs

OM protein - protein search, using sw model

Run on: January 12, 2006, 16:10:35 ; Search time 65 Seconds
(without alignments)
54.271 Million cell updates/sec

Title: US-10-716-030-1
Perfect score: 24
Sequence: 1 LNRRA 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	100.0	60	2	Q08090_SYNSP	Q08090 synechococc
2	24	100.0	72	2	Q853W6_9CAUD	Q853w6 mycobacteri
3	24	100.0	86	2	Q5P816_AZOSE	Q5p816 azoarcus sp
4	24	100.0	96	2	Q7Q4A8_ANOGA	Q7q4a8 anopheles g
5	24	100.0	97	2	Q8FE20_ECOL6	Q8fe20 escherichia
6	24	100.0	98	2	Q8VUX4_STAHO	Q8vux4 staphylococ
7	24	100.0	98	2	Q9LBZ5_STAAU	Q9lbz5 staphylococ
8	24	100.0	98	2	Q6GD55_STAAS	Q6gd55 staphylococ
9	24	100.0	98	2	Q5HJV3_STAAC	Q5hjv3 staphylococ
10	24	100.0	100	1	HIS1_KLEPN	P05148 klebsiella
11	24	100.0	109	2	Q5YXR3_NOCFA	Q5yxr3 nocardia fa
12	24	100.0	110	2	Q9F5L4_BRAJA	Q9f514 bradyrhizob
13	24	100.0	114	2	Q6F4B4_TRASC	Q6f4b4 trachemys s
14	24	100.0	117	2	Q4P9X2_USTMA	Q4p9x2 ustilago ma
15	24	100.0	117	2	Q9P071_HUMAN	Q9p071 homo sapien
16	24	100.0	118	2	Q4L1G1_9CAUD	Q4l1g1 burkholderi
17	24	100.0	121	2	Q71I70_LACDL	Q71i70 lactobacill
18	24	100.0	124	2	Q6F4B3_TRASC	Q6f4b3 trachemys s
19	24	100.0	138	2	Q9TTG7_AOTLE	Q9ttg7 aotus lemur
20	24	100.0	138	2	Q4S586_TETNG	Q4s586 tetraodon n
21	24	100.0	139	2	Q7XYL8_CHLS6	Q7xyl8 chlorarachn
22	24	100.0	139	2	Q7NFX2_GLOVI	Q7nfx2 gloeobacter
23	24	100.0	143	2	Q51YE7_MAGGR	Q51ye7 magnaporthe
24	24	100.0	144	2	Q4UXC3_XANCP	Q4uxc3 xanthomonas
25	24	100.0	144	2	Q87EZ5_XYLFT	Q87ez5 xylella fas
26	24	100.0	144	2	Q9PGW4_XYLFA	Q9pgw4 xylella fas
27	24	100.0	144	2	Q8P6T7_XANCP	Q8p6t7 xanthomonas
28	24	100.0	145	2	Q5LQC4_SILPO	Q5lqc4 silicibacte
29	24	100.0	147	2	Q602F2_METCA	Q602f2 methylococc
30	24	100.0	148	2	Q8SWQ2_ENCCU	Q8swq2 encephalito
31	24	100.0	149	2	O97538_AOTVO	O97538 aotus vocif
32	24	100.0	149	2	O97543_AOTNA	O97543 aotus nancy
33	24	100.0	149	2	Q9TTG8_AOTNI	Q9ttg8 aotus nigri
34	24	100.0	150	2	Q8LRS2_SORAU	Q8lrs2 sorbus aucu
35	24	100.0	155	2	Q8HZD5_SAGOE	Q8hzd5 saguinus oe
36	24	100.0	155	2	Q8HZD7_PONPY	Q8hzd7 pongo pygma
37	24	100.0	155	2	Q8HZD8_9PRIM	Q8hzd8 gorilla gor
38	24	100.0	156	2	Q4TJP7_9SPHN	Q4tjp7 erythrobact
39	24	100.0	157	2	Q5NUW1_9BURK	Q5nuw1 ralstonia m
40	24	100.0	158	2	Q4NJ46_9MICC	Q4nj46 arthrobacte
41	24	100.0	158	2	Q6MM44_BDEBA	Q6mm44 bdellovibri
42	24	100.0	161	2	Q4PNZ2_GLOAC	Q4pnz2 glomerella
43	24	100.0	169	2	Q6DQL8_MAIZE	Q6dql8 zea mays (m
44	24	100.0	173	2	Q6F9C6_ACIAD	Q6f9c6 acinetobact
45	24	100.0	179	2	Q7XJ85_PYRCO	Q7xj85 pyrus commu

ALIGNMENTS

RESULT 1
Q08090_SYNSP
ID Q08090_SYNSP PRELIMINARY; PRT; 60 AA.
AC Q08090;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CpeB, cpeA genes and ORF3 (Fragment).
OS Synechococcus sp.
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=1131;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94207193; PubMed=7512390;
RA Newman J., Mann N.H., Carr N.G.;
RT "Organization and transcription of the class I phycoerythrin genes of the marine cyanobacterium Synechococcus sp. WH7803.";
RL Plant Mol. Biol. 24:679-683(1994).
DR EMBL; X72961; CAA51463.1; -; Genomic_DNA.
DR PIR; S43777; S43777.
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6678 MW; 8773BCE2E82BECAC CRC64;

Query Match 100.0%; Score 24; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 20 LNRRA 24

RESULT 2
Q853W6_9CAUD
ID Q853W6_9CAUD PRELIMINARY; PRT; 72 AA.
AC Q853W6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp200.
GN Name=200;
OS Mycobacteriophage Omega.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=205879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22592660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;
RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C., Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R., Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S., Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W., Hatfull G.F.;
RT "Origins of highly mosaic mycobacteriophage genomes.";
RL Cell 113:171-182(2003).

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DR   EMBL; AY129338; AAN12842.1; -; Genomic_DNA.
SQ   SEQUENCE   72 AA;  8042 MW;  A38DAC1C5529B6F1 CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 72;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         16 LNRRA 20


RESULT 3
Q5P816_AZOSE
ID   Q5P816_AZOSE PRELIMINARY;      PRT;    86 AA.
AC   Q5P816;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=AZOSEA04230; ORFNames=ebA808;
OS   Azoarcus sp. (strain EbN1).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;
OC   Rhodocyclaceae; Azoarcus.
OX   NCBI_TaxID=76114;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=EbN1;
RX   PubMed=15551059; DOI=10.1007/s00203-004-0742-9;
RA   Rabus R., Kube M., Heider J., Beck A., Heitmann K., Widdel F.,
RA   Reinhardt R.;
RT   "The genome sequence of an anaerobic aromatic-degrading denitrifying
RT   bacterium, strain EbN1.";
RL   Arch. Microbiol. 183:27-36(2005).
DR   EMBL; CR555306; CAI06545.1; -; Genomic_DNA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   86 AA;  9410 MW;  ADA604AEFEFBB8CF CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 86;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         12 LNRRA 16


RESULT 4
Q7Q4A8_ANOGA
ID   Q7Q4A8_ANOGA PRELIMINARY;      PRT;    96 AA.
AC   Q7Q4A8;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ENSANGP00000018223.
GN   ORFNames=ENSANGG00000015734;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Anophelinae; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RT   "Anopheles gambiae re-annotation.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008964; EAA12199.2; -; Genomic_DNA.
DR   InterPro; IPR001562; BTK.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR011993; PH_type.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
DR   PROSITE; PS51113; ZF_BTK; 1.
KW   Metal-binding; Zinc; Zinc-finger.
SQ   SEQUENCE   96 AA;  11216 MW;  6ECE774DC9CBCE26 CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 96;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         68 LNRRA 72


RESULT 5
Q8FE20_ECOL6
ID   Q8FE20_ECOL6 PRELIMINARY;      PRT;    97 AA.
AC   Q8FE20;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein c3549.
GN   OrderedLocusNames=c3549;
OS   Escherichia coli O6.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=217992;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX   MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA   Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA   Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA   Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA   Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT   "Extensive mosaic structure revealed by the complete genome sequence
RT   of uropathogenic Escherichia coli.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR   EMBL; AE016766; AAN81997.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   97 AA;  10945 MW;  138BDBF80ACF67E5 CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 97;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         91 LNRRA 95


RESULT 6
Q8VUX4_STAHO
ID   Q8VUX4_STAHO PRELIMINARY;      PRT;    98 AA.
AC   Q8VUX4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ORF12.
OS   Staphylococcus hominis.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=1290;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=GIFU12263;
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RX   MEDLINE=22586405; PubMed=12700250;
RX   DOI=10.1128/JB.185.9.2711-2722.2003;
RA   Katayama Y., Takeuchi F., Ito T., Ma X.X., Ui-Mizutani Y.,
RA   Kobayashi I., Hiramatsu K.;
RT   "Identification in methicillin-susceptible Staphylococcus hominis of
RT   an active primordial mobile genetic element for the staphylococcal
RT   cassette chromosome mec of methicillin-resistant Staphylococcus
RT   aureus.";
RL   J. Bacteriol. 185:2711-2722(2003).
DR   EMBL; AB063171; BAB83483.1; -; Genomic_DNA.
DR   InterPro; IPR010813; DUF1413.
DR   Pfam; PF07205; DUF1413; 1.
SQ   SEQUENCE   98 AA;  11104 MW;  2B95AB85279039C9 CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         34 LNRRA 38


RESULT 7
Q9LBZ5_STAAU
ID   Q9LBZ5_STAAU PRELIMINARY;      PRT;    98 AA.
AC   Q9LBZ5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Staphylococcus aureus.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=1280;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NCTC10442;
RX   MEDLINE=21199321; PubMed=11302791;
RX   DOI=10.1128/AAC.45.5.1323-1336.2001;
RA   Ito T., Katayama Y., Asada K., Mori N., Tsutsumimoto K.;
RT   "Structural comparison of three types of staphylococcal cassette
RT   chromosome mec integrated in the chromosome in methicillin-resistant
RT   Staphylococcus aureus.";
RL   Antimicrob. Agents Chemother. 45:1323-1336(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NCTC10442;
RA   Ito T., Okuma K., Xue M.X., Yuzawa H., Hiramatsu K.;
RT   "Insights on antibiotic resistance of Staphylococcus aureus from its
RT   whole genome: genomic island SCC.";
RL   Drug Resist. Updat. 6:41-52(2003).
DR   EMBL; AB033763; BAA94325.1; -; Genomic_DNA.
DR   InterPro; IPR010813; DUF1413.
DR   Pfam; PF07205; DUF1413; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   98 AA;  11149 MW;  DCCF9E59FFF8AE0A CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         34 LNRRA 38


RESULT 8
Q6GD55_STAAS
ID   Q6GD55_STAAS PRELIMINARY;      PRT;    98 AA.
AC   Q6GD55;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=SAS0035;
OS   Staphylococcus aureus (strain MSSA476).
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=282459;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA   Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA   Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA   Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA   Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA   Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA   James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA   Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.,
RA   Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA   Spratt B.G., Parkhill J.;
RT   "Complete genomes of two clinical Staphylococcus aureus strains:
RT   evidence for the rapid evolution of virulence and drug resistance.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR   EMBL; BX571857; CAG41807.1; -; Genomic_DNA.
DR   InterPro; IPR010813; DUF1413.
DR   Pfam; PF07205; DUF1413; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   98 AA;  11109 MW;  8D5577B576DE82C6 CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         34 LNRRA 38


RESULT 9
Q5HJV3_STAAC
ID   Q5HJV3_STAAC PRELIMINARY;      PRT;    98 AA.
AC   Q5HJV3;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=SACOL0044;
OS   Staphylococcus aureus (strain COL).
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=93062;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
RA   Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA   Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA   Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA   Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,
RA   Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA   Hance I.R., Nelson K.E., Fraser C.M.;
RT   "Insights on evolution of virulence and resistance from the complete
RT   genome analysis of an early methicillin-resistant Staphylococcus
RT   aureus strain and a biofilm-producing methicillin-resistant
RT   Staphylococcus epidermidis strain.";
RL   J. Bacteriol. 187:2426-2438(2005).
DR   EMBL; CP000046; AAW38693.1; -; Genomic_DNA.
DR   TIGR; SACOL0044; -.
DR   InterPro; IPR010813; DUF1413.
DR   Pfam; PF07205; DUF1413; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   98 AA;  11149 MW;  DCCF9E59FFF8AE0A CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
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              |||||
Db         34 LNRRA 38


RESULT 10
HIS1_KLEPN
ID   HIS1_KLEPN     STANDARD;      PRT;   100 AA.
AC   P05148;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   ATP phosphoribosyltransferase (EC 2.4.2.17) (ATP-PRTase) (ATP-PRT)
DE   (Fragment).
GN   Name=hisG;
OS   Klebsiella pneumoniae.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Klebsiella.
OX   NCBI_TaxID=573;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=84135578; PubMed=6321433;
RA   Rodriguez R.L., West R.W. Jr.;
RT   "Histidine operon control region of Klebsiella pneumoniae: analysis
RT   with an Escherichia coli promoter-probe plasmid vector.";
RL   J. Bacteriol. 157:764-771(1984).
CC   -!- FUNCTION: Catalyzes the condensation of ATP and PRPP to form N'-
CC       5'-phosphoribosyl-ATP (PR-ATP). Has a crucial role in the pathway
CC       because the rate of histidine biosynthesis seems to be controlled
CC       primarily by regulation of hisG enzymatic activity (By
CC       similarity).
CC   -!- CATALYTIC ACTIVITY: 1-(5-phospho-D-ribosyl)-ATP + diphosphate =
CC       ATP + 5-phospho-alpha-D-ribose 1-diphosphate.
CC   -!- COFACTOR: Magnesium (By similarity).
CC   -!- ENZYME REGULATION: Feedback inhibited by histidine (By
CC       similarity).
CC   -!- PATHWAY: Amino-acid biosynthesis; L-histidine biosynthesis; L-
CC       histidine from PRPP: step 1.
CC   -!- SUBUNIT: Equilibrium between an active dimeric form, an inactive
CC       hexameric form and higher aggregates. Interconversion between the
CC       various forms is largely reversible and is influenced by the
CC       natural substrates and inhibitors of the enzyme (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: Belongs to the ATP phosphoribosyltransferase family.
CC       Long subfamily.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; K01997; AAA25073.1; -; Genomic_DNA.
DR   SMR; P05148; 5-100.
DR   HAMAP; MF_00079; -; 1.
DR   InterPro; IPR001348; ATP_phspho_trans.
DR   Pfam; PF01634; HisG; 1.
DR   PROSITE; PS01316; ATP_P_PHORIBOSYLTR; PARTIAL.
KW   Amino-acid biosynthesis; Glycosyltransferase; Histidine biosynthesis;
KW   Magnesium; Metal-binding; Transferase.
FT   NON_TER     100    100
SQ   SEQUENCE   100 AA;  11408 MW;  BDA8FEB042E012DE CRC64;

  Query Match             100.0%;  Score 24;  DB 1;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         82 LNRRA 86


RESULT 11
Q5YXR3_NOCFA
ID   Q5YXR3_NOCFA PRELIMINARY;      PRT;   109 AA.
AC   Q5YXR3;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative transcriptional regulator.
GN   OrderedLocusNames=nfa21810;
OS   Nocardia farcinica.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Corynebacterineae; Nocardiaceae; Nocardia.
OX   NCBI_TaxID=37329;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=IFM 10152;
RX   PubMed=15466710; DOI=10.1073/pnas.0406410101;
RA   Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
RA   Shiba T., Hattori M.;
RT   "The complete genomic sequence of Nocardia farcinica IFM 10152.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
DR   EMBL; AP006618; BAD57028.1; -; Genomic_DNA.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0006350; P:transcription; IEA.
DR   InterPro; IPR001845; HTH_ArsR.
DR   InterPro; IPR011991; Wing_hlx_DNA_bd.
DR   Pfam; PF01022; HTH_5; 1.
DR   PRINTS; PR00778; HTHARSR.
DR   SMART; SM00418; HTH_ARSR; 1.
DR   PROSITE; PS50987; HTH_ARSR_2; 1.
KW   Cadmium resistance; Complete proteome; DNA-binding; Transcription;
KW   Transcription regulation.
SQ   SEQUENCE   109 AA;  12758 MW;  C8E8C003FB725173 CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         73 LNRRA 77


RESULT 12
Q9F5L4_BRAJA
ID   Q9F5L4_BRAJA PRELIMINARY;      PRT;   110 AA.
AC   Q9F5L4; Q79U54;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   NapD (Periplasmic nitrate reductase).
GN   Name=napD; OrderedLocusNames=blr7037;
OS   Bradyrhizobium japonicum.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Bradyrhizobiaceae; Bradyrhizobium.
OX   NCBI_TaxID=375;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=110spc4;
RX   PubMed=14663073; DOI=10.1099/mic.0.26620-0;
RA   Delgado M., Bonnard N., Tresierra-Ayala A., Bedmar E.J., Muller P.;
RT   "The Bradyrhizobium japonicum napEDABC genes encoding the periplasmic
RT   nitrate reductase are essential for nitrate respiration.";
RL   Microbiology 149:3395-3403(2003).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=110spc4;
RA   Mueller P.;
RT   "The putative napD napA operon of Bradyrhizobium japonicum 110spc4.";
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=USDA 110;
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RX   MEDLINE=22484998; PubMed=12597275;
RA   Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA   Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA   Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA   Tabata S.;
RT   "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT   Bradyrhizobium japonicum USDA110.";
RL   DNA Res. 9:189-197(2002).
DR   EMBL; AF314590; AAG31647.1; -; Genomic_DNA.
DR   EMBL; BA000040; BAC52302.1; -; Genomic_DNA.
DR   InterPro; IPR005623; NapD.
DR   Pfam; PF03927; NapD; 1.
KW   Complete proteome.
SQ   SEQUENCE   110 AA;  11787 MW;  9546CE2C46FC0BDB CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         12 LNRRA 16


RESULT 13
Q6F4B4_TRASC
ID   Q6F4B4_TRASC PRELIMINARY;      PRT;   114 AA.
AC   Q6F4B4;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Preproghrelin-1 precursor.
OS   Trachemys scripta elegans.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.
OX   NCBI_TaxID=31138;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Stomach;
RX   PubMed=15242751; DOI=10.1016/j.ygcen.2004.05.005;
RA   Kaiya H., Sakata I., Kojima M., Hosoda H., Sakai T., Kangawa K.;
RT   "Structural determination and histochemical localization of ghrelin in
RT   the red-eared slider turtle, Trachemys scripta elegans.";
RL   Gen. Comp. Endocrinol. 138:50-57(2004).
DR   EMBL; AB161457; BAD29730.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
DR   InterPro; IPR005441; Preproghrelin.
DR   PANTHER; PTHR14122; Preproghrelin; 1.
DR   PRINTS; PR01624; GHRELIN.
DR   ProDom; PD332162; Preproghrelin; 1.
KW   Signal.
FT   SIGNAL        1     23       Potential.
FT   CHAIN        24     48       ghrelin.
SQ   SEQUENCE   114 AA;  13300 MW;  07DE5E24BF9DEDF2 CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         47 LNRRA 51


RESULT 14
Q4P9X2_USTMA
ID   Q4P9X2_USTMA PRELIMINARY;      PRT;   117 AA.
AC   Q4P9X2;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Predicted protein.
GN   ORFNames=UM03091.1;
OS   Ustilago maydis 521.
OC   Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC   Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX   NCBI_TaxID=237631;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=521;
RA   Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA   Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA   Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA   Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA   Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
RA   Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA   Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA   David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA   Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA   Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA   Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA   Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA   Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA   Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA   Jaffe D., Jones C., Kamal M., Kamat A., Kamvysselis M., Karlsson E.,
RA   Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
RA   Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA   Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
RA   Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA   Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA   Mccarthy M., Mcdonough S., Mcghee T., Meldrim J., Meneus L.,
RA   Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA   Mozes J., Mulrain L., Munson G., Naylor J., Newes C., Nguyen C.,
RA   Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA   Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA   O'neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piqani B.,
RA   Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA   Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA   Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA   Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA   Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA   Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA   Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA   Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA   Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA   Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA   Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA   Zimmer A., Zody M., Lander E.;
RT   "The genome sequence of Ustilago maydis.";
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AACP01000104; EAK83882.1; -; Genomic_DNA.
SQ   SEQUENCE   117 AA;  12734 MW;  357E4480E3118265 CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         93 LNRRA 97


RESULT 15
Q9P071_HUMAN
ID   Q9P071_HUMAN PRELIMINARY;      PRT;   117 AA.
AC   Q9P071;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   HSPC311 (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Blood;
RA   Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
RA   Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF161429; AAF28989.1; -; mRNA.
FT   NON_TER       1       1
SQ   SEQUENCE   117 AA;  13276 MW;  246F7F794620AAFF CRC64;

  Query Match             100.0%;  Score 24;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LNRRA 5
              |||||
Db         80 LNRRA 84


Search completed: January 12, 2006, 16:18:43
Job time : 67 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 12, 2006, 16:12:05 ; Search time 11.5 Seconds
(without alignments)
41.833 Million cell updates/sec

Title: US-10-716-030-1
Perfect score: 24
Sequence: 1 LNRRA 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	100.0	60	2	S43777	hypothetical prote
2	24	100.0	122	2	E69980	hypothetical prote
3	24	100.0	144	2	H82837	conserved hypothet
4	24	100.0	189	2	S04670	hypothetical prote
5	24	100.0	194	2	JS0664	interferon precurs
6	24	100.0	233	1	QWHUN	tumor necrosis fac
7	24	100.0	233	1	S22052	tumor necrosis fac
8	24	100.0	237	2	C87656	GGDEF family prote
9	24	100.0	247	2	E87283	tRNA pseudouridine
10	24	100.0	255	2	AG3435	guanylate kinase (
11	24	100.0	259	2	G95890	probable transcrip
12	24	100.0	278	2	S77601	hypothetical prote
13	24	100.0	285	2	I38248	steroidogenic acut
14	24	100.0	285	2	JC4315	steroidogenic acut
15	24	100.0	287	2	F70788	hypothetical prote
16	24	100.0	299	1	XREBT	ATP phosphoribosyl
17	24	100.0	299	1	XREC	ATP phosphoribosyl
18	24	100.0	299	2	AC0764	ATP phosphoribosyl
19	24	100.0	299	2	D90981	ATP phosphoribosyl
20	24	100.0	299	2	B85827	ATP phosphoribosyl
21	24	100.0	299	2	AI0188	ATP phosphoribosyl
22	24	100.0	304	2	AI3285	geranyltranstransf
23	24	100.0	306	2	AC2649	ABC transporter, m
24	24	100.0	310	2	I46987	bone sialoprotein
25	24	100.0	319	2	I60446	Shiga-like cytotox
26	24	100.0	325	2	D37476	fiber - human aden
27	24	100.0	337	2	B97431	alpha-glucosides t
28	24	100.0	338	2	T36307	hypothetical prote
29	24	100.0	341	2	T46153	hypothetical prote
30	24	100.0	343	2	T50179	yeast bud pattern
31	24	100.0	362	2	JC5386	steroidogenic acut
32	24	100.0	386	2	B75516	conserved hypothet
33	24	100.0	398	2	E70621	probable argG prot
34	24	100.0	399	2	F87085	arginosuccinate sy
35	24	100.0	415	2	C84698	hypothetical prote
36	24	100.0	430	2	AI2624	hypothetical prote
37	24	100.0	430	2	H97406	hypothetical prote
38	24	100.0	434	2	T50800	hypothetical prote
39	24	100.0	439	2	A42289	glucose-fructose o
40	24	100.0	443	2	B82209	GGDEF family prote
41	24	100.0	453	2	T15374	hypothetical prote
42	24	100.0	461	2	AC0005	probable membrane
43	24	100.0	463	2	AC0969	probable purine pe
44	24	100.0	463	2	C86042	probable transport
45	24	100.0	463	2	B91195	probable transport

ALIGNMENTS

RESULT 1
S43777
hypothetical protein 3 - Synechococcus sp.
C;Species: Synechococcus sp.
C;Date: 10-Dec-1994 #sequence_revision 26-May-1995 #text_change 05-Oct-2004
C;Accession: S43777; S32640
R;Newman, J.; Mann, N.H.; Carr, N.G.
Plant Mol. Biol. 24, 679-683, 1994
A;Title: Organization and transcription of the class I phycoerythrin genes of the marin
A;Reference number: S43777; MUID:94207193; PMID:7512390
A;Accession: S43777
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-60 <NEW>
A;Cross-references: UNIPROT:Q08090; UNIPARC:UPI00000BBC83; EMBL:X72961; NID:g288983; PI
A;Note: the authors translated the codon CAC for residue 27 as His
C;Superfamily: uncharacterized conserved protein

Query Match 100.0%; Score 24; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 20 LNRRA 24

RESULT 2
E69980
hypothetical protein yrvB - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: E69980
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: E69980
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Residues: 1-122 <KUN>
A;Cross-references: UNIPARC:UPI000006082B; GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CA
A;Experimental source: strain 168
C;Genetics:
A;Gene: yrvB

Query Match 100.0%; Score 24; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 68 LNRRA 72

RESULT 3
H82837
conserved hypothetical protein XF0184 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: H82837
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: H82837
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-144 <SIM>
A;Cross-references: UNIPROT:Q9PGW4; UNIPARC:UPI00000C2313; GB:AE003872; GB:AE003849; NID
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laign
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0184

Query Match 100.0%; Score 24; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 84 LNRRA 88

RESULT 4
S04670
hypothetical protein 5 - Rhodopseudomonas blastica
C;Species: Rhodopseudomonas blastica
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S04670
R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription.
A;Reference number: S04666; MUID:85058188; PMID:6209404
A;Accession: S04670
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-189 <TYB>
A;Cross-references: UNIPROT:P05448; UNIPARC:UPI000013A168

Query Match 100.0%; Score 24; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 5 LNRRA 9

RESULT 5
JS0664
interferon precursor - cat
C;Species: Felis silvestris catus (domestic cat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JS0664
R;Nakamura, N.; Sudo, T.; Matsuda, S.; Yanai, A.
Biosci. Biotechnol. Biochem. 56, 211-214, 1992
A;Title: Molecular cloning of feline interferon cDNA by direct expression.
A;Reference number: JS0664; MUID:92323151; PMID:1377975
A;Accession: JS0664
A;Molecule type: mRNA
A;Residues: 1-194 <NAK>
A;Cross-references: UNIPROT:P35849; UNIPARC:UPI000012D64A
C;Superfamily: interferon alpha
C;Keywords: glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-194/Product: interferon #status predicted <INT>
F;102/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 24; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 33 LNRRA 37

RESULT 6
QWHUN
tumor necrosis factor alpha precursor [validated] - human
N;Alternate names: cachectin; TNFA
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004
C;Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23
R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D
Nucleic Acids Res. 13, 6361-6373, 1985
A;Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chrc
A;Reference number: A93585; MUID:86016093; PMID:2995927
A;Accession: A93585
A;Molecule type: DNA
A;Residues: 1-233 <NED>
A;Cross-references: UNIPROT:P01375; UNIPARC:UPI000000D745; GB:X02910; GB:X02159; NID:g37
R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka
Nature Genet. 3, 137-145, 1993
A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
A;Reference number: S36152; MUID:93272029; PMID:8499947
A;Accession: S36153
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-233 <IRI>
A;Cross-references: UNIPARC:UPI000000D745; EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.
Nature 312, 724-729, 1984
A;Title: Human tumour necrosis factor: precursor structure, expression and homology to l
A;Reference number: A93351; MUID:85086244; PMID:6392892
A;Accession: A93351
A;Molecule type: mRNA
A;Residues: 1-233 <PEN>
A;Cross-references: UNIPARC:UPI000000D745; GB:X02910; GB:X02159; NID:g37209; PIDN:CAA266
A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyelc

R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.;
Science 228, 149-154, 1985
A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A;Reference number: A44189; MUID:85142190; PMID:3856324
A;Accession: A44189
A;Molecule type: mRNA
A;Residues: 1-62,'S',64-233 <WAN>
A;Cross-references: UNIPARC:UPI000002FB8A; GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:
R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; Ar
Lymphokine Res. 7, 175-185, 1988
A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A;Reference number: A61478; MUID:88301617; PMID:2841543
A;Accession: B61478
A;Molecule type: protein
A;Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180
A;Cross-references: UNIPARC:UPI00001735C7; UNIPARC:UPI00001735C8; UNIPARC:UPI00001735C9;
R;Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
Eur. J. Biochem. 152, 515-522, 1985
A;Title: Molecular cloning and expression of human tumor necrosis factor and comparison
A;Reference number: I53311; MUID:86030296; PMID:3932069
A;Accession: I53311
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-233 <MAR>
A;Cross-references: UNIPARC:UPI000000D745; GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:
A;Experimental source: U-937 cells
R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
A;Reference number: S62610; MUID:96202967; PMID:8631363
A;Accession: S62610
A;Molecule type: protein
A;Residues: 77-99 <TAK>
A;Cross-references: UNIPARC:UPI00001735CD
R;D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter regic
A;Reference number: I54522; MUID:94102809; PMID:7903959
A;Accession: I54522
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-8 <DAL>
A;Cross-references: UNIPARC:UPI00001735CE; GB:S68530; NID:g544751
R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A;Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lys
A;Reference number: A59163; MUID:93018820; PMID:1402651
A;Contents: annotation; identification of myristylated lysines
R;Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bring
J. Biol. Chem. 260, 2345-2354, 1985
A;Title: Human tumor necrosis factor. Production, purification, and characterization.
A;Reference number: A92511; MUID:85130974; PMID:3871770
A;Contents: annotation; disulfide bond
C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction
out detriment to normal cells. It can also act synergistically with interferon gamma to
C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely
ut are produced by different cell types and have different induction kinetics.
C;Genetics:
A;Gene: GDB:TNF; TNFA
A;Cross-references: GDB:120441; OMIM:191160
A;Map position: 6p21.3-6p21.3
A;Introns: 62/3; 78/1; 94/1
C;Complex: homotrimer
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macr
F;1-76/Domain: propeptide #status predicted <PRO>
F;77-233/Product: tumor necrosis factor #status experimental <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental
F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F;145-177/Disulfide bonds: #status experimental

Query Match 100.0%; Score 24; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 105 LNRRA 109

RESULT 7
S22052
tumor necrosis factor alpha precursor - baboon
C;Species: Papio sp. (baboon)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S22052
R;Sanjanwala, M.; Edwards, A.
submitted to the EMBL Data Library, September 1991
A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A;Reference number: S22052
A;Accession: S22052
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <SAN>
A;Cross-references: UNIPROT:P33620; UNIPARC:UPI00001370C4; EMBL:X62141; NID:g38159; PIDN
C;Genetics:
A;Introns: 62/3; 78/1; 94/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;145-177/Disulfide bonds: #status predicted

Query Match 100.0%; Score 24; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 105 LNRRA 109

RESULT 8
C87656
GGDEF family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: C87656
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87656
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-237 <STO>
A;Cross-references: UNIPROT:Q9A3B9; UNIPARC:UPI00000C7A08; GB:AE005673; NID:g13424977;
C;Genetics:
A;Gene: CC3285

Query Match 100.0%; Score 24; DB 2; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 92 LNRRA 96

RESULT 9
E87283
tRNA pseudouridine synthase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004

C;Accession: E87283
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87283
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-247 <STO>
A;Cross-references: UNIPROT:Q9ABF0; UNIPARC:UPI00000D4535; GB:AE005673; NID:g13421415; P
C;Genetics:
A;Gene: CC0278
C;Superfamily: tRNA-pseudouridine synthase A, prokaryotic type

Query Match 100.0%; Score 24; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 116 LNRRA 120

RESULT 10
AG3435
guanylate kinase (EC 2.7.4.8) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AG3435
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AG3435
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-255 <KUR>
A;Cross-references: UNIPARC:UPI00000580A3; GB:AE008917; PIDN:AAL52650.1; PID:g17983473;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1469
A;Map position: I
C;Keywords: phosphotransferase

Query Match 100.0%; Score 24; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 180 LNRRA 184

RESULT 11
G95890
probable transcription regulator protein [imported] - Sinorhizobium meliloti (strain 102
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: G95890
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: G95890
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <KUR>
A;Cross-references: UNIPROT:Q92WE9; UNIPARC:UPI00000CB4F5; GB:AL591985; PIDN:CAC48791.1;
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMb20405
A;Genome: plasmid

Query Match 100.0%; Score 24; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 82 LNRRA 86

RESULT 12
S77601
hypothetical protein 278 - Paracoccus denitrificans
C;Species: Paracoccus denitrificans
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 09-Jul-2004
C;Accession: S77601
R;de Gier, J.W.; Schepper, M.; Reijnders, W.N.M.; van Dyck, S.J.; Slotboom, D.J.; Warne,
Mol. Microbiol. 20, 1247-1260, 1996
A;Title: Structural and functional analysis of aa(3)-type and cbb(3)-type cytochrome c o
A;Reference number: S77595; MUID:96405647; PMID:8809776
A;Accession: S77601
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-278 <DEA>
A;Cross-references: UNIPROT:Q51678; UNIPARC:UPI00000AF7F3; EMBL:U34353; NID:g1002874; PI
A;Experimental source: strain Pd1222
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995

Query Match 100.0%; Score 24; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 232 LNRRA 236

RESULT 13
I38248
steroidogenic acute regulatory protein - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38248; I38896
R;Sugawara, T.; Lin, D.; Holt, J.A.; Martin, K.O.; Javitt, N.B.; Miller, W.L.; Strauss,
Biochemistry 34, 12506-12512, 1995
A;Title: Structure of the human steroidogenic acute regulatory protein (StAR) gene: StAR
A;Reference number: I38248; MUID:96038208; PMID:7547998
A;Accession: I38248
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-285 <RES>
A;Cross-references: UNIPROT:P49675; UNIPARC:UPI000003AD93; EMBL:U29105; NID:g1041696; PI
R;Sugawara, T.; Holt, J.A.; Driscoll, D.; Strauss III, J.F.; Lin, D.; Miller, W.L.; Patt
Proc. Natl. Acad. Sci. U.S.A. 92, 4778-4782, 1995
A;Title: Human steroidogenic acute regulatory protein: functional activity in COS-1 cell
A;Reference number: I38896; MUID:95281540; PMID:7761400
A;Accession: I38896
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-285 <RE2>
A;Cross-references: UNIPARC:UPI000003AD93; EMBL:U17280; NID:g727252; PIDN:AAC50141.1; PI
C;Genetics:

A;Gene: StAR
A;Cross-references: GDB:STAR; GDB:635457; OMIM:600617
A;Map position: 8p11.2-8p11.2
A;Introns: 22/1; 60/1; 102/3; 155/3; 217/2; 248/3

Query Match 100.0%; Score 24; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 35 LNRRA 39

RESULT 14
JC4315
steroidogenic acute regulatory protein - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4315
R;Hartung, S.; Rust, W.; Balvers, M.; Ivell, R.
Biochem. Biophys. Res. Commun. 215, 646-653, 1995
A;Title: Molecular cloning and in vivo expression of the bovine steroidogenic acute regu
A;Reference number: JC4315; MUID:96011827; PMID:7488004
A;Accession: JC4315
A;Molecule type: mRNA
A;Residues: 1-285 <HAR>
A;Cross-references: UNIPROT:Q28918; UNIPARC:UPI0000136090
C;Comment: This protein is an acute controller of the rate-limiting transfer ofcholester
C;Genetics:
A;Gene: StAR
F;226-264/Region: metalloproteinase-1 tissue inhibitor similarity

Query Match 100.0%; Score 24; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 35 LNRRA 39

RESULT 15
F70788
hypothetical protein Rv3661 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Dec-2004
C;Accession: F70788
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70788
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-287 <COL>
A;Cross-references: UNIPROT:O69629; UNIPARC:UPI0000139267; GB:AL022121; GB:AL123456; NID
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv3661
C;Superfamily: phosphoserine phosphatase

Query Match 100.0%; Score 24; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRA 5
|||||
Db 55 LNRRA 59

Search completed: January 12, 2006, 16:19:17
Job time : 13.5 secs